



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:22 AM UTC

PDB ID : 8V83 / pdb_00008v83
EMDB ID : EMD-43017
Title : 60S ribosome biogenesis intermediate (Dbp10 pre-catalytic structure - Overall map)
Authors : Cruz, V.E.; Weirich, C.S.; Peddada, N.; Erzberger, J.P.
Deposited on : 2023-12-04
Resolution : 2.53 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

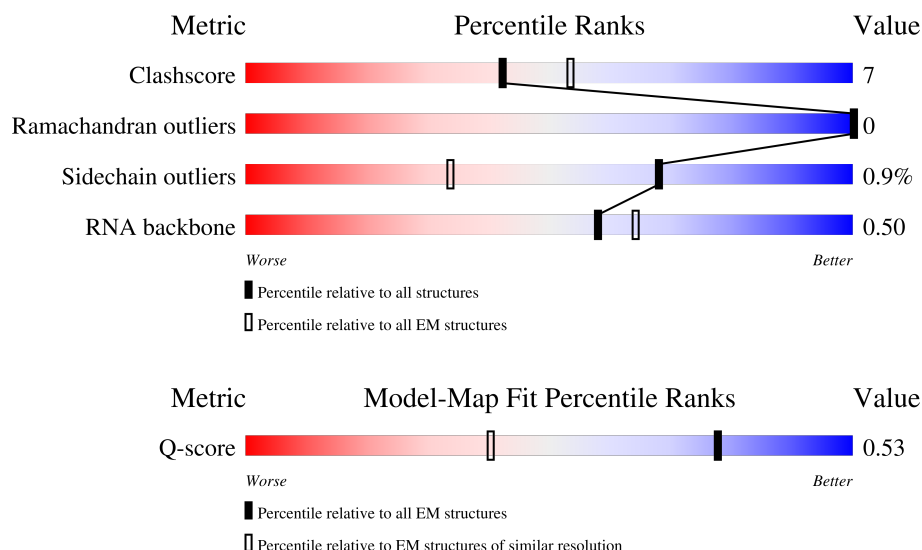
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

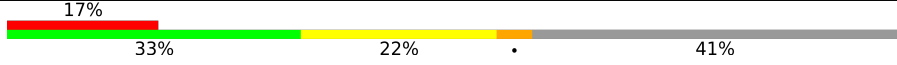
The reported resolution of this entry is 2.53 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7309 (2.03 - 3.03)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3396	
2	2	158	
3	6	232	

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Mol	Chain	Length	Quality of chain
4	7	204	
5	8	434	
6	A	291	
7	B	387	
8	C	362	
9	D	505	
10	E	176	
11	F	244	
12	G	256	
13	H	191	
14	I	463	
15	J	427	
16	K	376	
17	L	199	
18	M	138	
19	N	204	
20	O	199	
21	P	184	
22	Q	186	
23	R	306	
24	S	172	
25	T	250	
26	V	137	
27	W	236	
28	Y	127	

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Mol	Chain	Length	Quality of chain
29	Z	453	
30	a	217	
31	b	647	
32	e	130	
33	f	107	
34	h	120	
35	i	100	
36	j	88	
37	l	181	
38	m	807	
39	n	605	
40	o	220	
41	q	618	
42	r	261	
43	t	322	
44	u	199	
45	v	231	
46	w	278	
47	x	295	
48	y	245	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 119224 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called *Saccharomyces cerevisiae* S288C 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2015	Total	C	N	O	P	0	0
			43147	19266	7811	14055	2015		

- Molecule 2 is a RNA chain called *Saccharomyces cerevisiae* S288C 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	150	Total	C	N	O	P	0	0
			3189	1426	563	1050	150		

- Molecule 3 is a RNA chain called *Saccharomyces cerevisiae* ITS-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	58	Total	C	N	O	P	0	0
			1227	550	210	409	58		

- Molecule 4 is a protein called 60S ribosomal subunit assembly/export protein LOC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	7	11	Total	C	N	O	0	0
			87	56	15	16		

- Molecule 5 is a protein called Ribosomal RNA-processing protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	8	143	Total	C	N	O	S	0	0
			1203	743	240	216	4		

- Molecule 6 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	255	Total	C	N	O	S	0	0
			2080	1326	372	376	6		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	331	Total	C	N	O	S	0	0
			2626	1669	484	467	6		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	343	Total	C	N	O	S	0	0
			2611	1643	499	466	3		

- Molecule 9 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	423	Total	C	N	O	S	0	0
			3377	2183	573	609	12		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	151	Total	C	N	O	S	0	0
			1205	780	215	209	1		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	241	Total	C	N	O	S	0	0
			1936	1246	351	338	1		

- Molecule 12 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	164	Total	C	N	O	S	0	0
			1272	818	217	235	2		

- Molecule 13 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	189	Total	C	N	O	S	0	0
			1502	952	272	275	3		

- Molecule 14 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	394	Total	C	N	O	S	0	0
			3126	1997	525	593	11		

- Molecule 15 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	151	Total	C	N	O	S	0	0
			1271	793	240	235	3		

- Molecule 16 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	268	Total	C	N	O	S	0	0
			2155	1387	355	409	4		

- Molecule 17 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	110	Total	C	N	O	S	0	0
			884	552	185	147			

- Molecule 18 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	134	Total	C	N	O	S	0	0
			1041	668	197	174	2		

- Molecule 19 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	177	Total	C	N	O	S	0	0
			1513	948	320	244	1		

- Molecule 20 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	188	Total	C	N	O	S	0	0
			1486	960	275	250	1		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	137	Total	C	N	O	0	0
			1062	666	198	198		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Q	144	Total	C	N	O	S	0
			1110	704	213	192	1	0

- Molecule 23 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	190	Total	C	N	O	S	0
			1578	996	297	275	10	0

- Molecule 24 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	S	170	Total	C	N	O	S	0
			1432	922	265	242	3	0

- Molecule 25 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	T	79	Total	C	N	O	0	0
			625	390	109	126		

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	V	114	Total	C	N	O	S	0
			845	535	154	149	7	0

- Molecule 27 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	W	232	Total	C	N	O	S	0
			1870	1184	321	360	5	0

- Molecule 28 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Y	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 29 is a protein called Ribosome biogenesis protein SSF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	253	Total	C	N	O	S	0	0
			2020	1280	361	370	9		

- Molecule 30 is a protein called Large ribosomal subunit protein uL1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	210	Total	C	N	O	S	0	0
			1668	1067	291	301	9		

- Molecule 31 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	423	Total	C	N	O	S	0	0
			3429	2193	586	632	18		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	126	Total	C	N	O	S	0	0
			1018	646	204	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 34 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 35 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	84	Total	C	N	O	S	0	0
			665	413	136	114	2		

- Molecule 36 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	72	Total	C	N	O	S	0	0
			571	347	124	95	5		

- Molecule 37 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	176	Total	C	N	O	S	0	0
			1394	896	244	247	7		

- Molecule 38 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	211	Total	C	N	O	S	0	0
			1759	1116	305	333	5		

- Molecule 39 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	337	Total	C	N	O	S	0	0
			2760	1804	462	486	8		

- Molecule 40 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 41 is a protein called 25S rRNA (cytosine(2870)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	358	Total	C	N	O	S	0	0
			2799	1779	490	518	12		

- Molecule 42 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	184	Total	C	N	O	S	0	0
			1489	937	286	261	5		

- Molecule 43 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	249	Total	C	N	O	S	0	0
			1973	1258	352	360	3		

- Molecule 44 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	112	Total	C	N	O	S	0	0
			944	594	191	150	9		

- Molecule 45 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	149	Total	C	N	O	S	0	0
			1242	778	242	219	3		

- Molecule 46 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	w	243	Total	C	N	O	S	0	0
			2058	1334	353	366	5		

- Molecule 47 is a protein called Ribosome production factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	279	Total	C	N	O	S	0	0
			2362	1500	427	431	4		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	225	Total	C	N	O	S	0	0
			1701	1056	295	343	7		

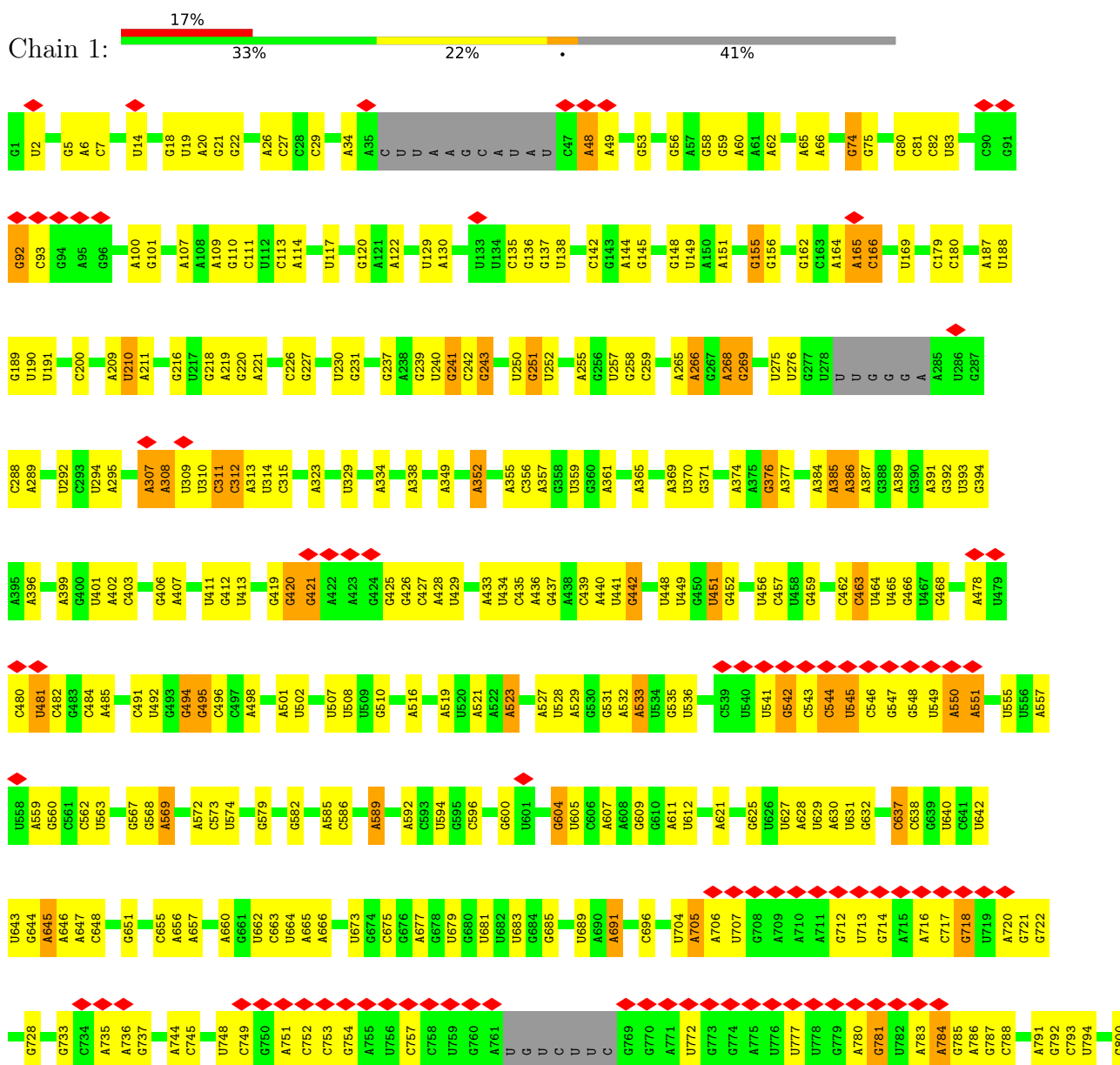
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

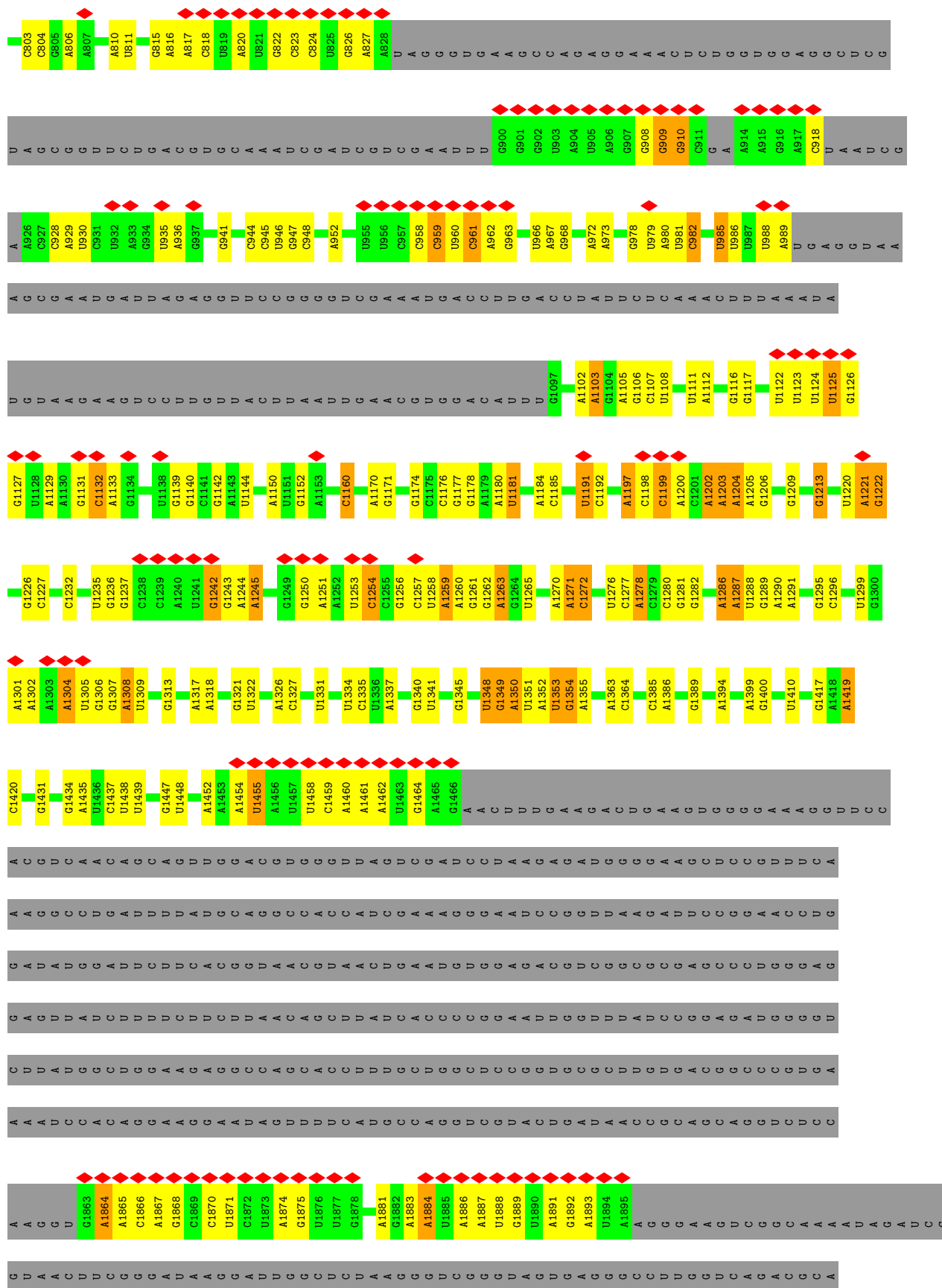
Mol	Chain	Residues	Atoms		AltConf
49	j	1	Total 1	Zn 1	0
49	u	1	Total 1	Zn 1	0

3 Residue-property plots

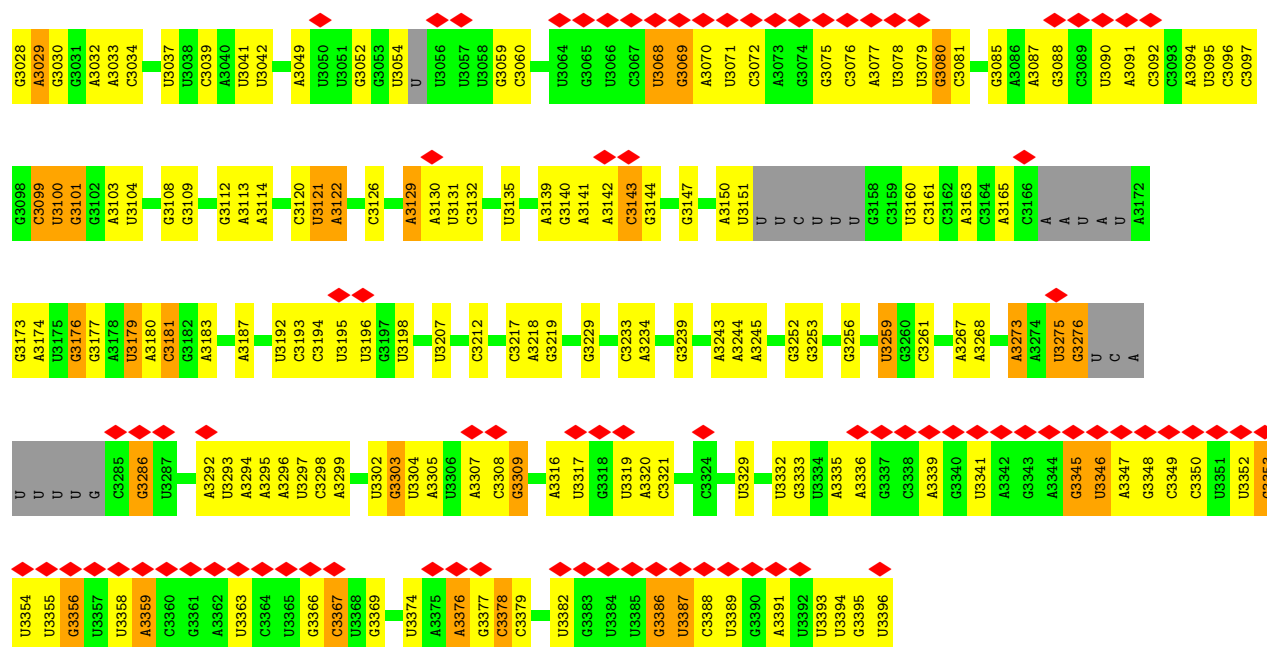
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: *Saccharomyces cerevisiae* S288C 25S ribosomal RNA

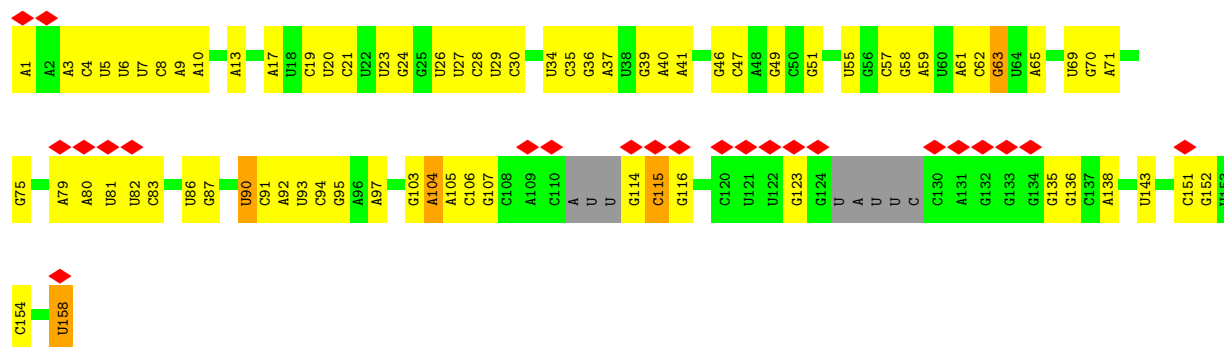




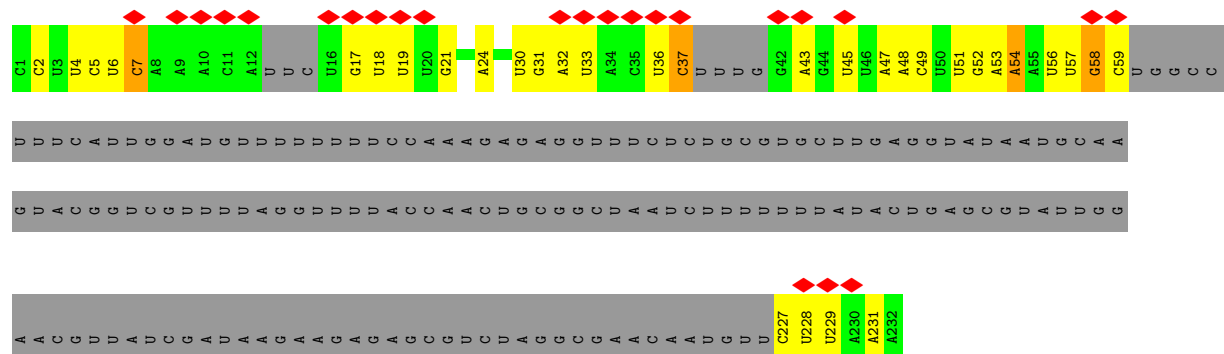




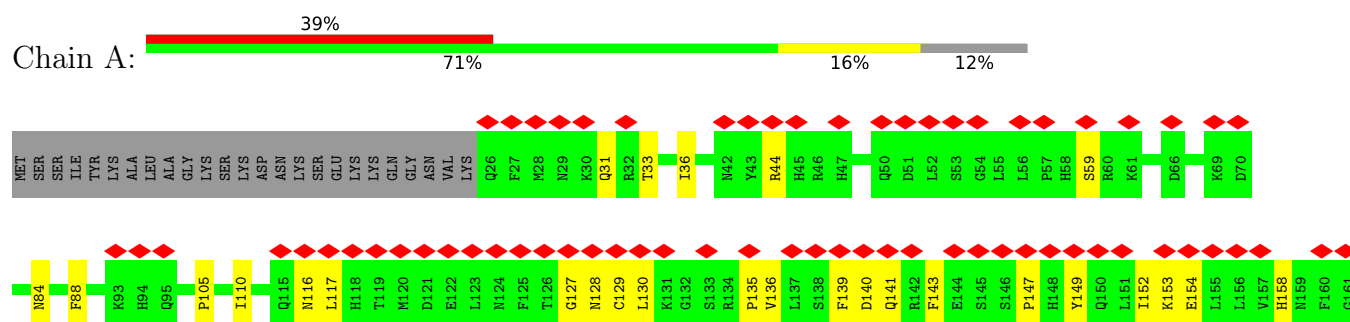
• Molecule 2: Saccharomyces cerevisiae S288C 5.8S ribosomal RNA

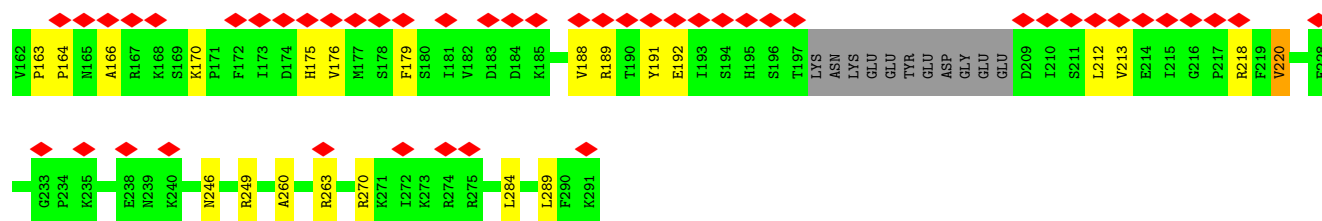


• Molecule 3: Saccharomyces cerevisiae ITS-2

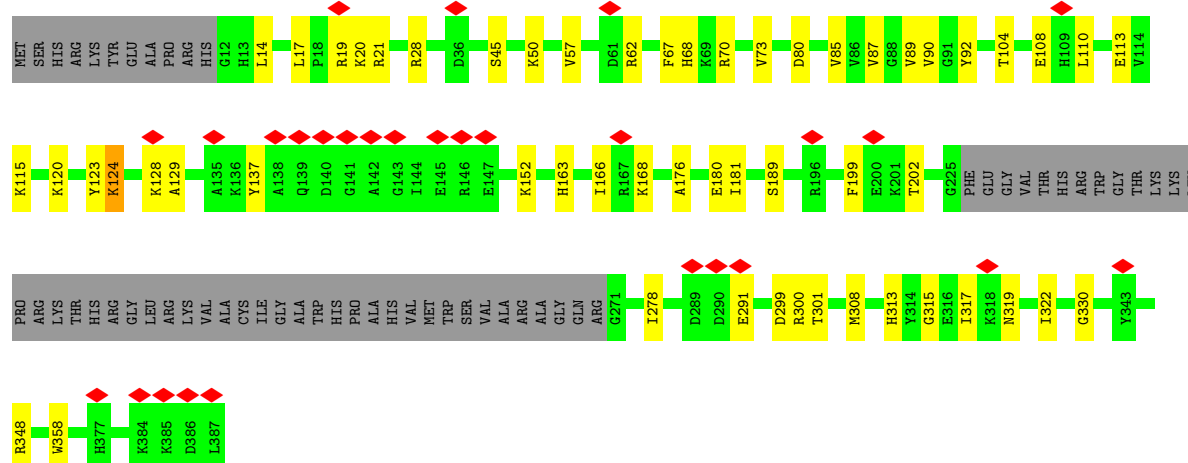


• Molecule 4: 60S ribosomal subunit assembly/export protein LOC1

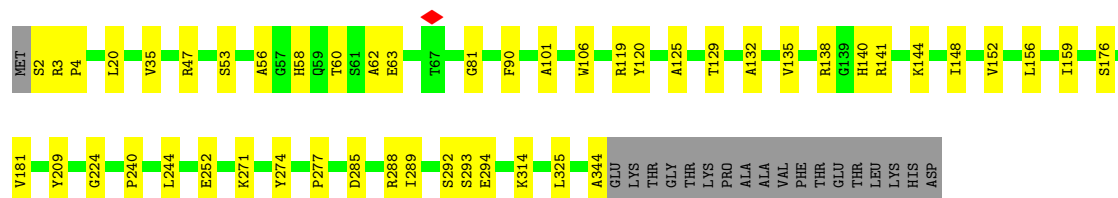
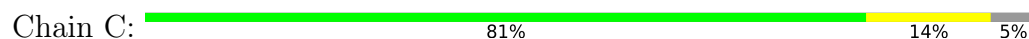




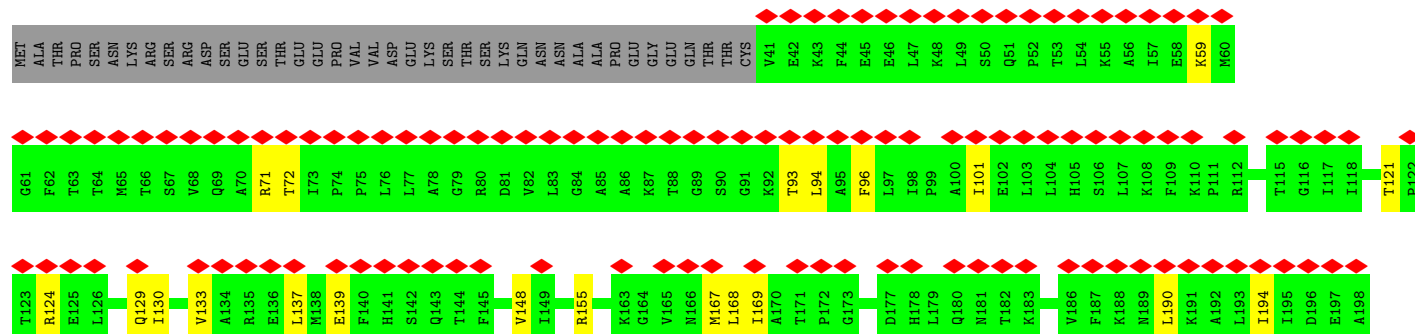
• Molecule 7: 60S ribosomal protein L3

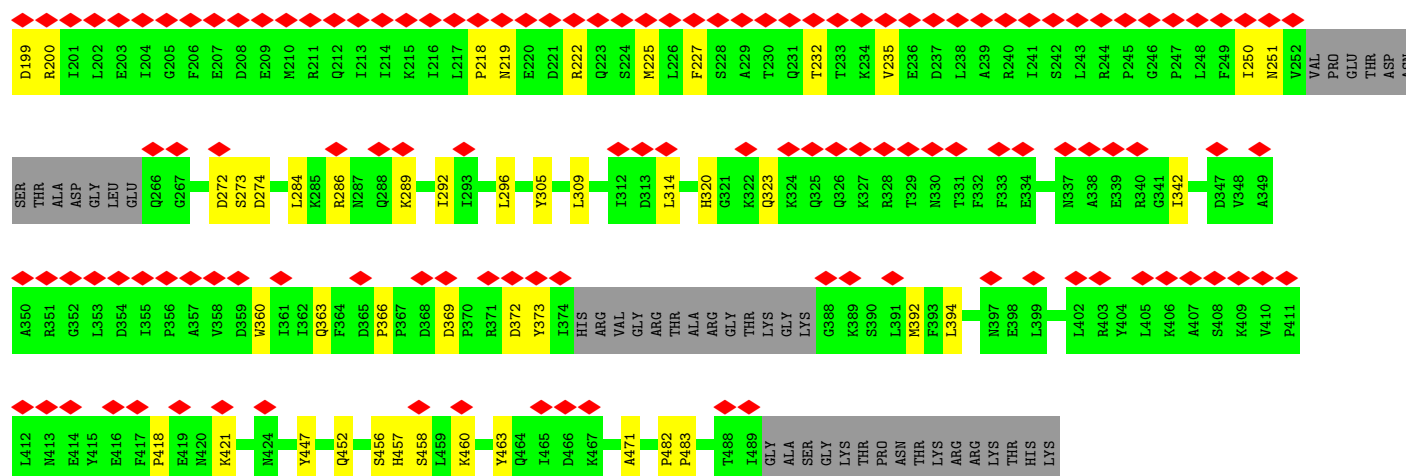


• Molecule 8: 60S ribosomal protein L4-A

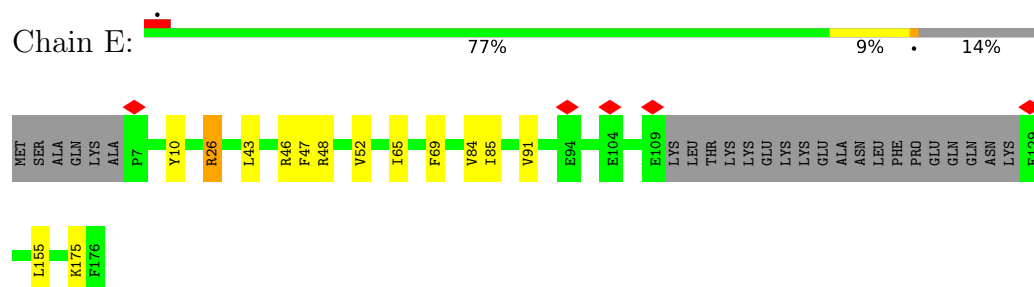


• Molecule 9: ATP-dependent RNA helicase HAS1

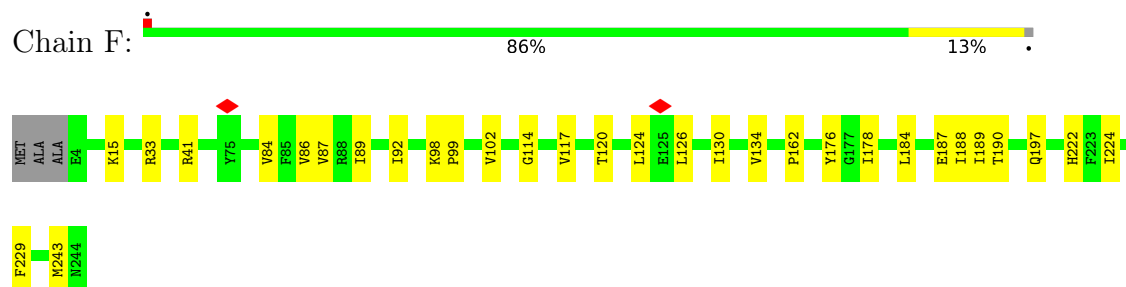




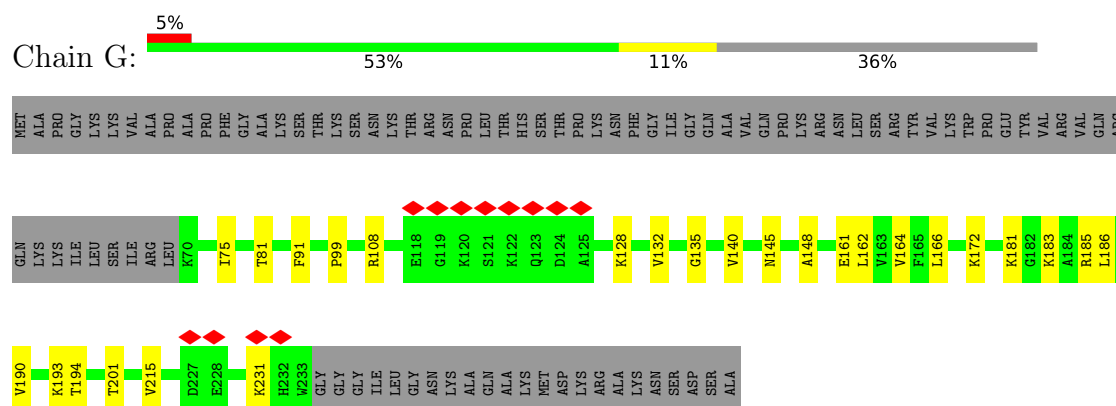
- Molecule 10: 60S ribosomal protein L6-A



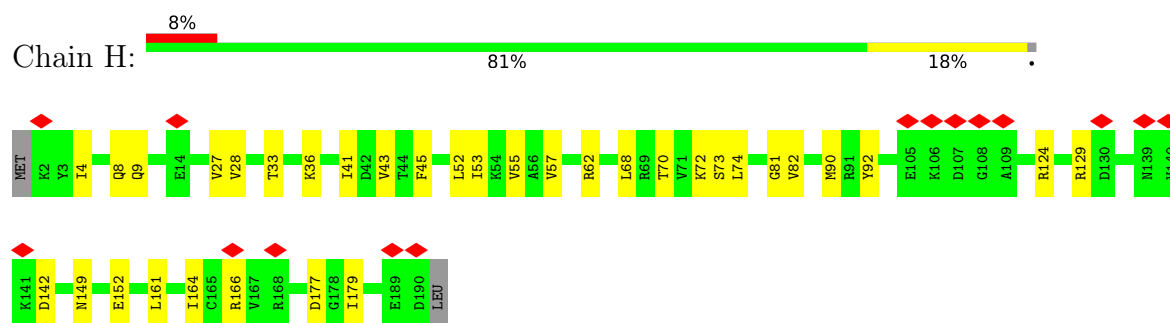
- Molecule 11: 60S ribosomal protein L7-A



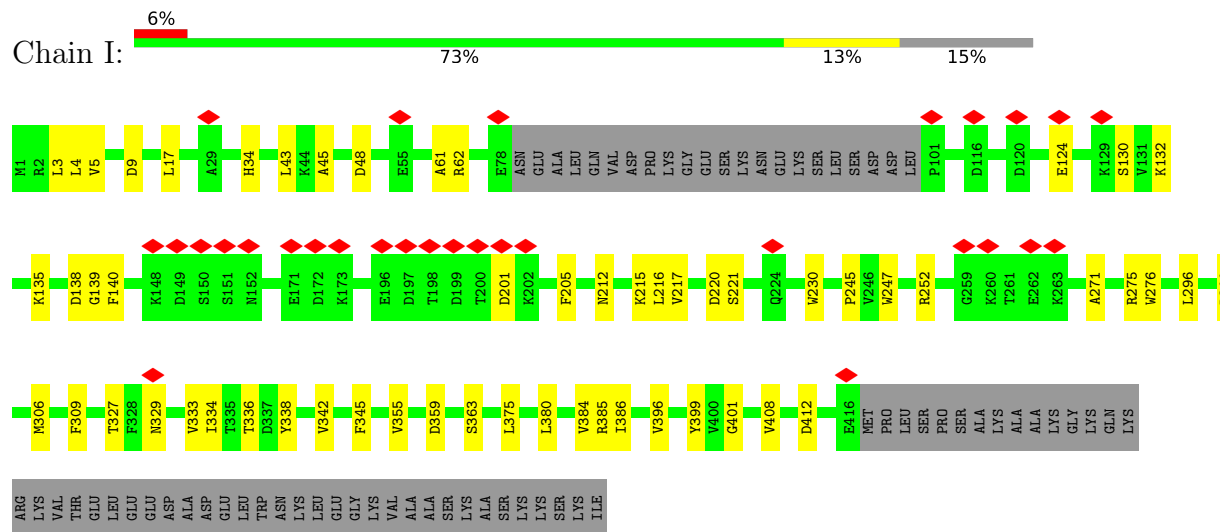
- Molecule 12: Large ribosomal subunit protein eL8A



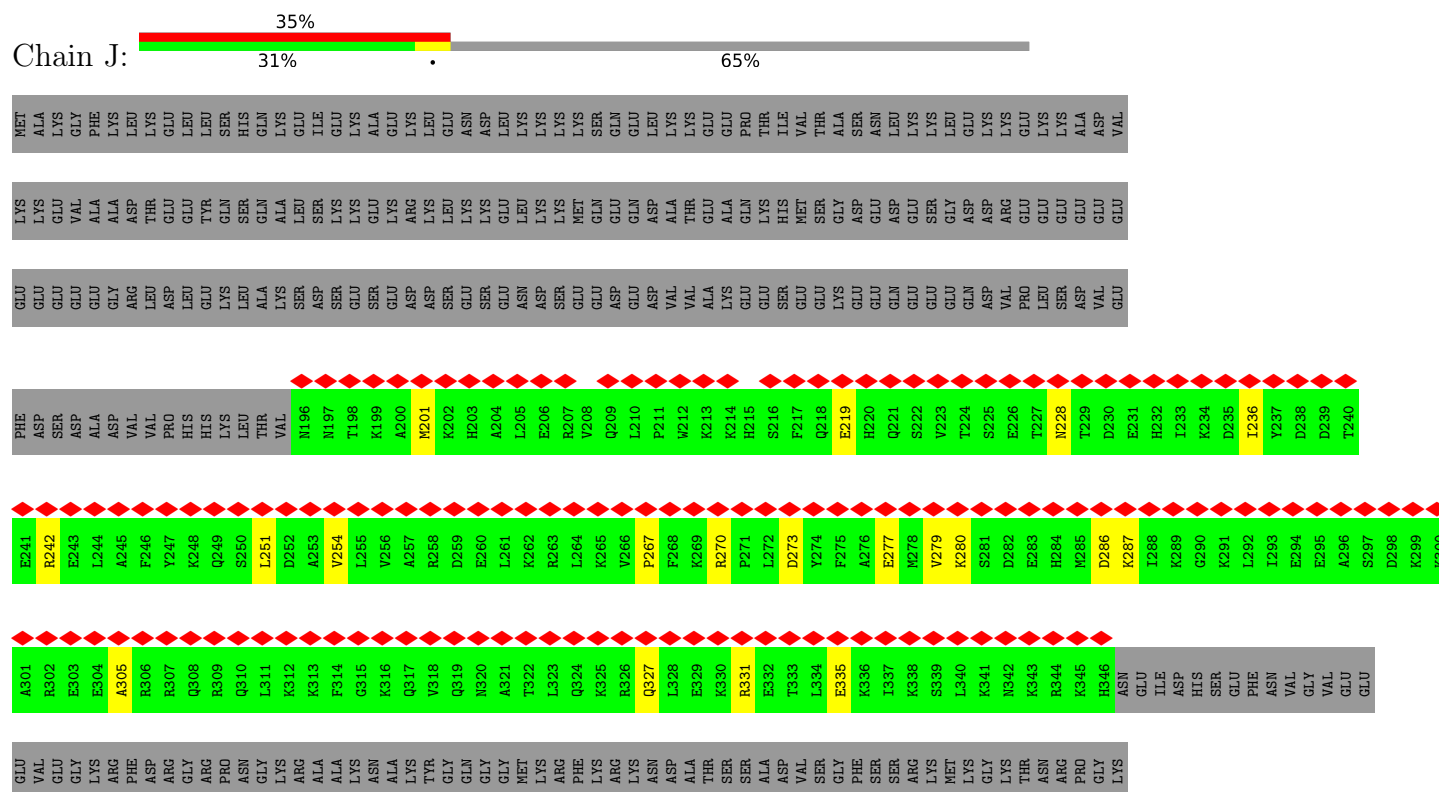
- Molecule 13: Large ribosomal subunit protein uL6A



• Molecule 14: Ribosome biogenesis protein NSA1



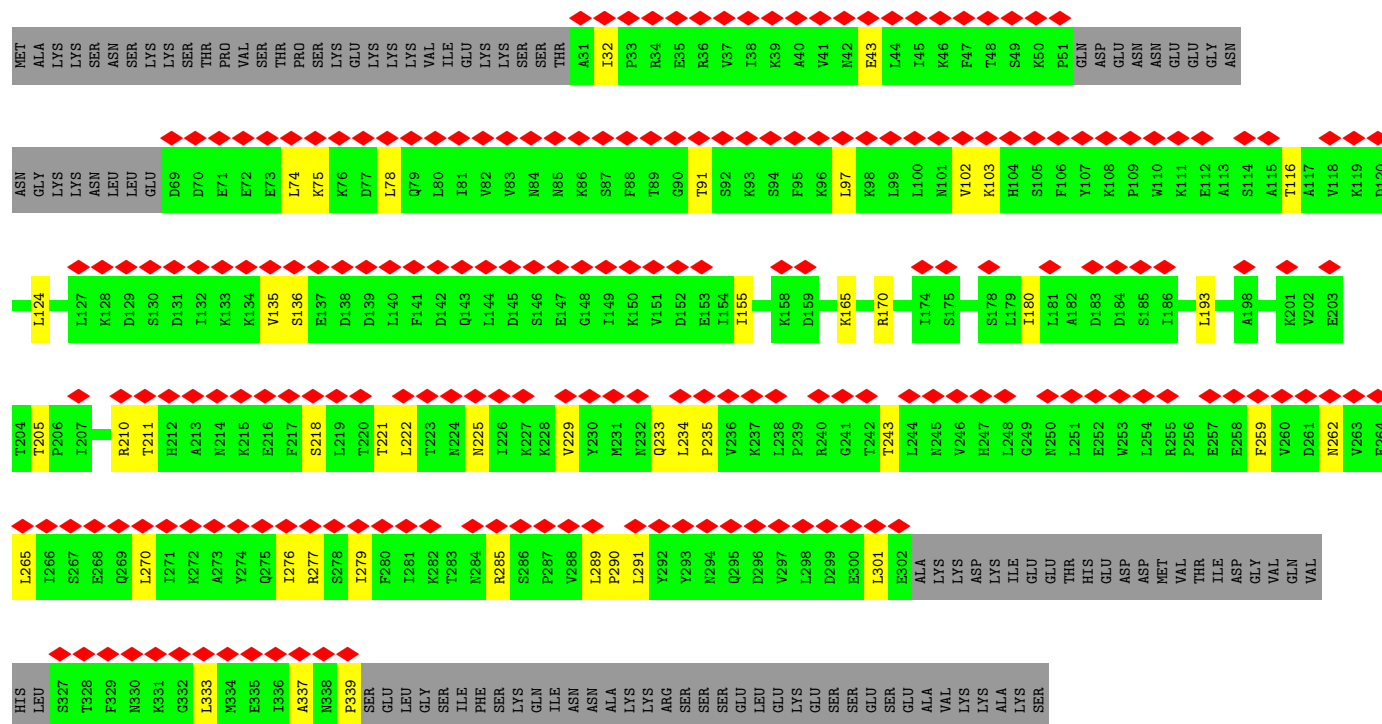
• Molecule 15: rRNA-processing protein EBP2



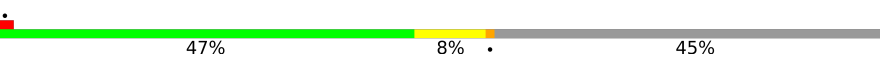
SER
ARG
LYS
ALA
ARG
ARG
PHE

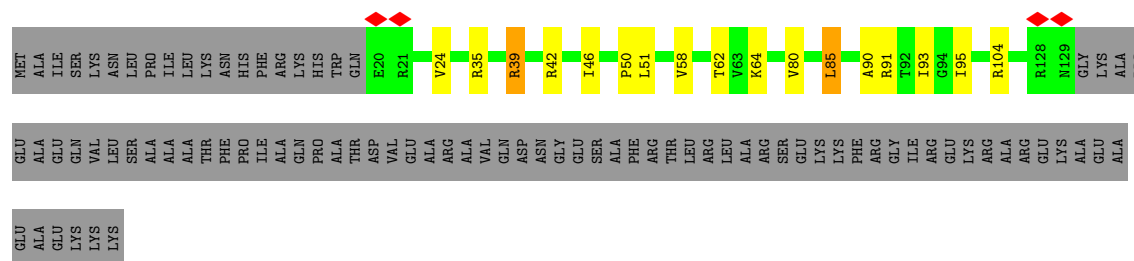
• Molecule 16: Proteasome-interacting protein CIC1

Chain K: 



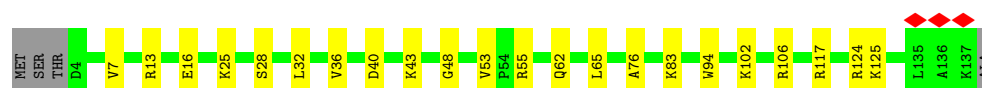
• Molecule 17: 60S ribosomal protein L13-A

Chain L: 

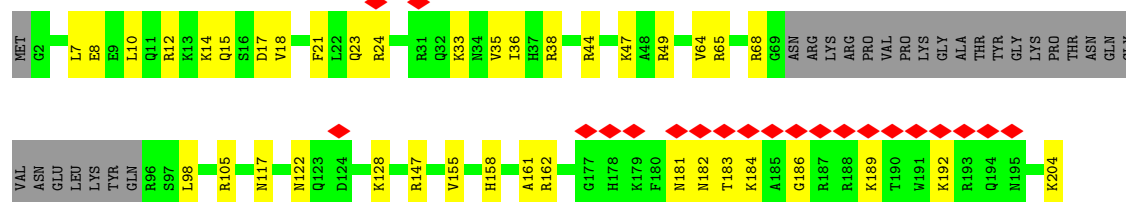


• Molecule 18: 60S ribosomal protein L14-A

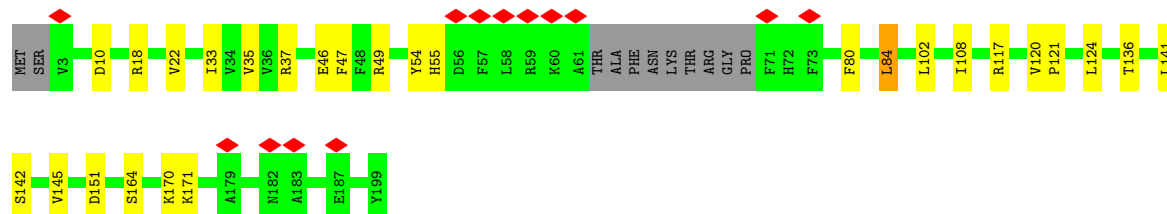
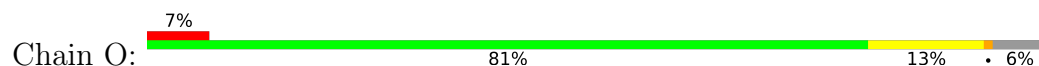
Chain M: 



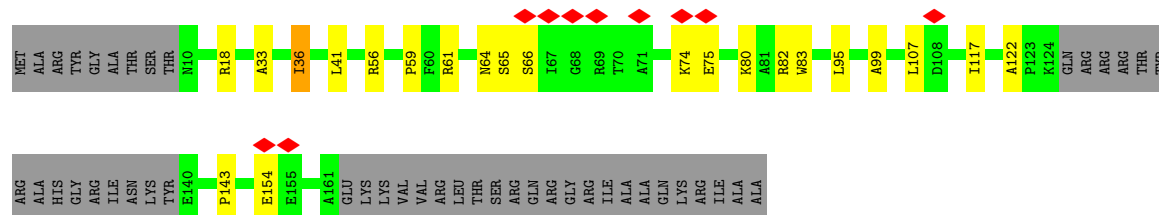
• Molecule 19: Large ribosomal subunit protein eL15A



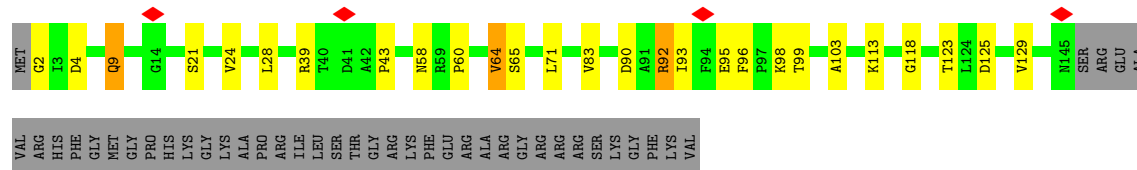
- Molecule 20: Large ribosomal subunit protein uL13A



- Molecule 21: 60S ribosomal protein L17-A



- Molecule 22: 60S ribosomal protein L18-A

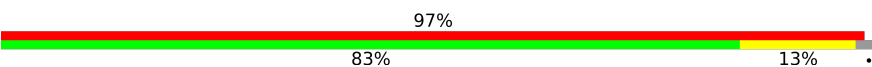


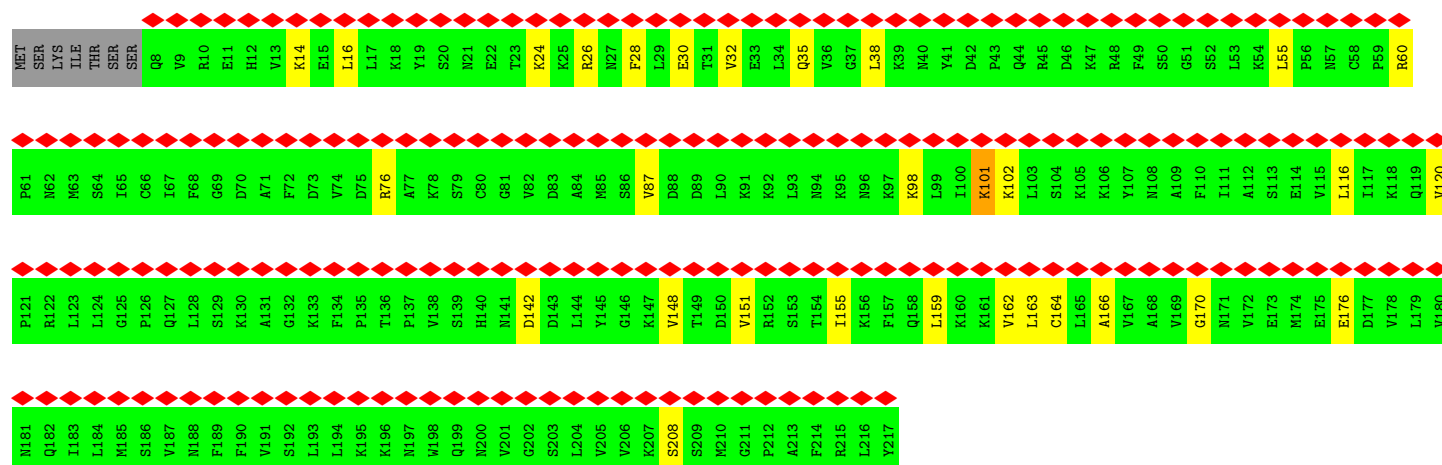
- Molecule 23: Protein MAK16



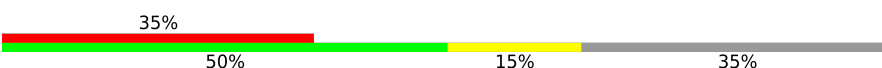
ASP ASP ALA MET MET SER ASP ASP GLU SER SER SER ASP ASP GLU HIS TVR GLY SER VAL PRO GLU ASP LEU ASP SER ASP PHE LEU VAL GLU

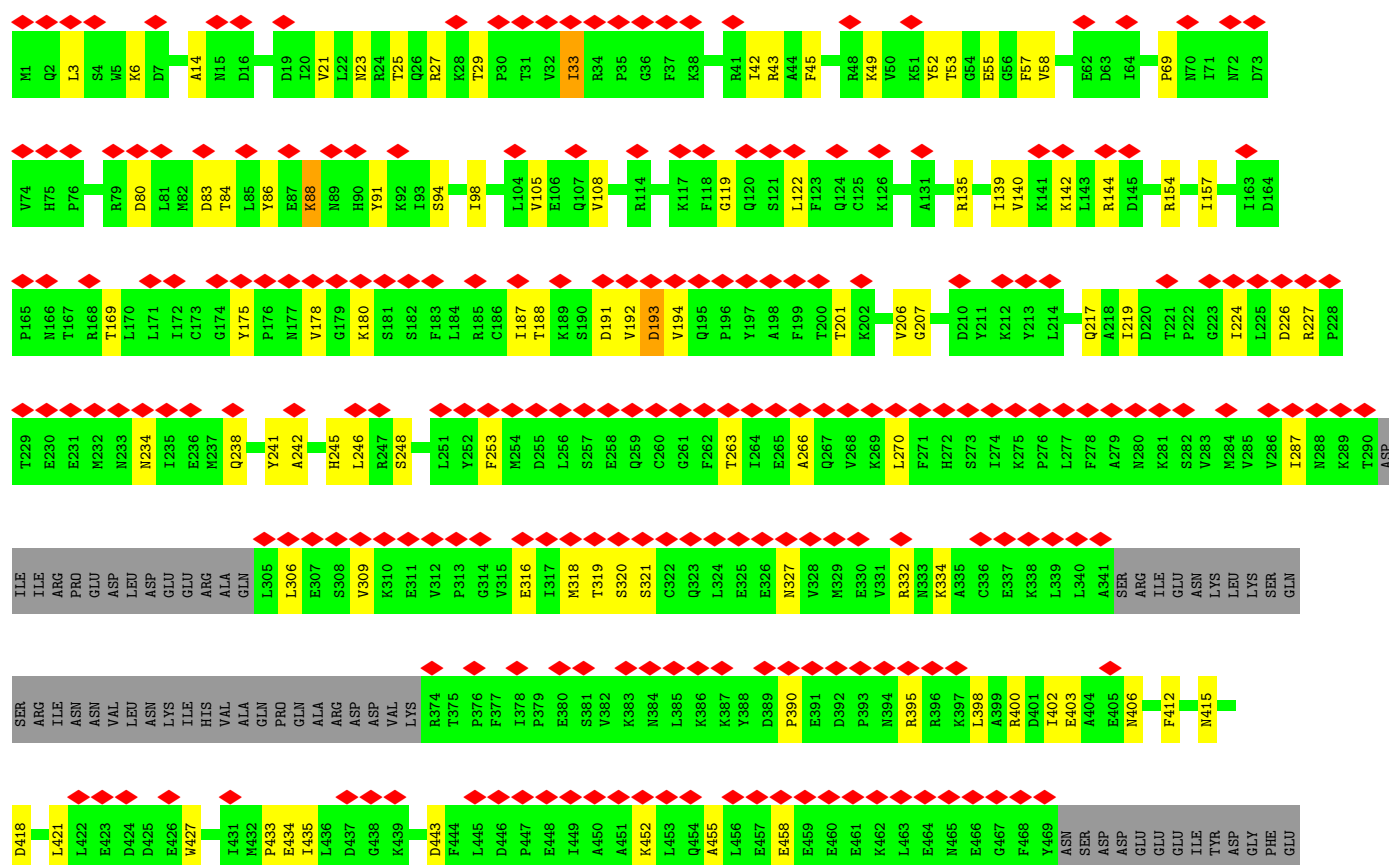
• Molecule 30: Large ribosomal subunit protein uL1A

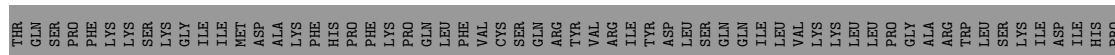
Chain a: 



• Molecule 31: Nucleolar GTP-binding protein 1

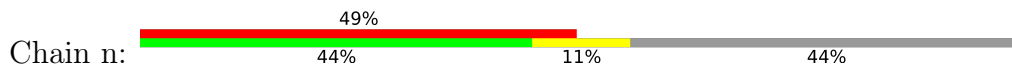
Chain b: 





HIS	ALA	THR	VAL	TYR	ASP	ASP	MET	MET	LYS	ASN	PRO	MET	ILE	VAL	PRO	PRO	LEU	LYS	LYS	VAL	ILE	ASN	ASN	SER	LEU	GLY	GLY	VAL	LEU	ASP	ALA	ALA	ILE	TRP	HIS	PRO	ARG	GLU	GLU	TRP	TRP	LEU	PHE	SER	ALA	GLY	ALA	ASP	ASN	THR	ALA	ARG	ALA	LEU	TRP	THR
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- Molecule 39: Pescadillo homolog



MET	ARG	ILE	LYS	LYS	LYS	ASN	THR	ARG	GLY	ASN	ALA	ARG	ASN	F15	I16	T17	R18	S19	Q20	A21	R22	K24	L25	Q26	T27	S28	L29	A30	D31	F32	R33	L35	C36	I37	F38	K39	G40	Y42	P43	ARG	GLU	PRO	ARG	ASN	LYS	LYS	SER	THR	ALA	PRO
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TBR
F62
Y63
Y64
A65
K66
D67
I68
Q69
Y70
L71
M72
H73
E74
F75
V76
L77
A78
K79
F80
R81
L90
V99
K103
R104
N108
R109
D110
S111
Y112
T113
L114
D115
H116
I117
I118
K119
E120
R121
Y122
P123
S124
F125
P126
D127
A128
I129
R130
D131
I132
D133
D134
A135
L136
N137
M138

L139	F140	L141	F142	L143	N144	L145	F146	L147	L148	L149	Q150	L151	L152	L153	L154	L155	L156	L157	L158	L159	Q160	L161	L162	C163	L164	Q165	L166	L167	L168	L169	V170	A171	L172	E173	R174	L175	V176	R177	R178	R179	F180	L181	S182	L183	L184	G185	L186	V187	L188	Q189	A190	N191	L192	L193	G194	E195	L196	V197	L198	L199	L200
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V201	P202	K203	F204	F205	P206	E207	L208	L209	P210	S211	D212	V213	D214	F215	R216	L217	M218	L219	L222	E223	F224	Y225	S226	T227	L228	L229	H230	F231	V232	L233	V234	K235	L236	T237	T238	D239	S240	G241	L242	L243	V244	P245	P246	K247	L248	D249	L250	K251	K252	D253	K254	L255	L256	S257	G258	L259	S260	S261
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[illegible]

GLN	GLU	LYS	GLU	GLN	ASN	GLU	GLU	THR	GLU	LEU	ASP	THR	PRE	GLU	ASP	ASN	ASN	LYS	ASN	LYS	GLY	ASP	ILE	LEU	ILE	GLN	PRO	SER	X351	X352	X353	X354	X355	X356	X357	X358	X359	X360	X361	X362	X363	X364	X365	X366	X367	X368	X369	X370	X371	X372	X373	X374	X375	X376	X377	X378	X379	X380	X381
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S382	C383	C384	C385	N386	V387	S388	S389	E390	A391	C392	C393	D394	Q395	I396	GLU	ASN	LYS	ASP	ILE	ASP	MET	S405	K406	V407	T408	H409	Q410	I411	V412	D413	R414	P415	V416	L417	K418	N419	K420	V421	A422	Q423	R424	T425	V426	I427	Q428	P429	Q430	W431	I432	F433	D434	C435	I436	N437	K438	C439	E440	I441
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[illegible]

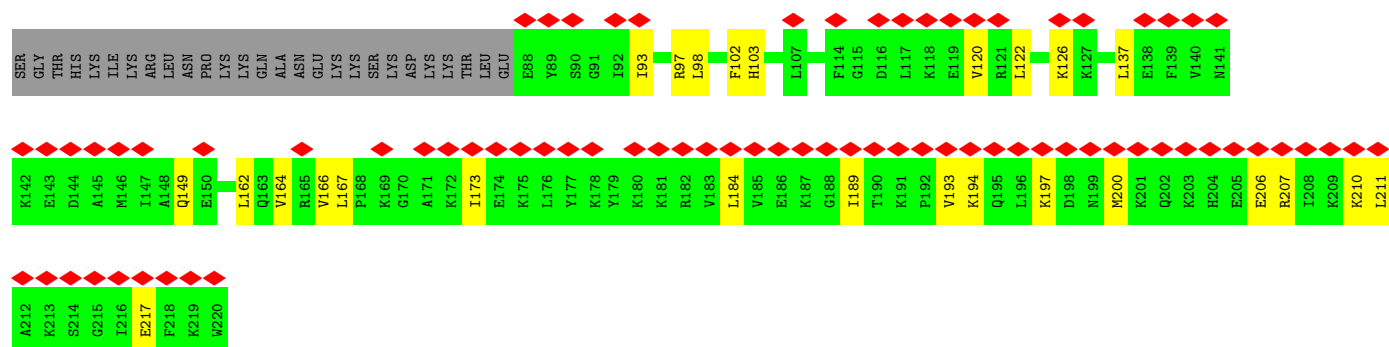
GLU ASP ASP ASP ASP ASP ASP GLU GLU LEU LEU ALA ALA LYS LYS SER SER THR THR SER SER GLU GLU ALA ALA LYS ASP ASP ASP VAL VAL ASN ASN LYS LYS SER SER LYS LYS ARG ARG LYS LYS VAL VAL ASP ASP GLU GLU GLU GLU LYS LYS LYS LYS LYS LYS MET MET MET MET SER SER ASN

LYS	GLN	LYS	LYS	LEU	TYR	LYS	MET	LYS	TYR	SER	ASN	ALA	LYS	LYS	GLU	GLU	GLN	ALA	GLU	ASN	LEU	LYS	LYS	LYS	LYS	GLN	ILE	ALA	LYS	GLN	LYS	ALA	LYS	ASN	LEU	LYS	ASP	SER	LYS	LYS
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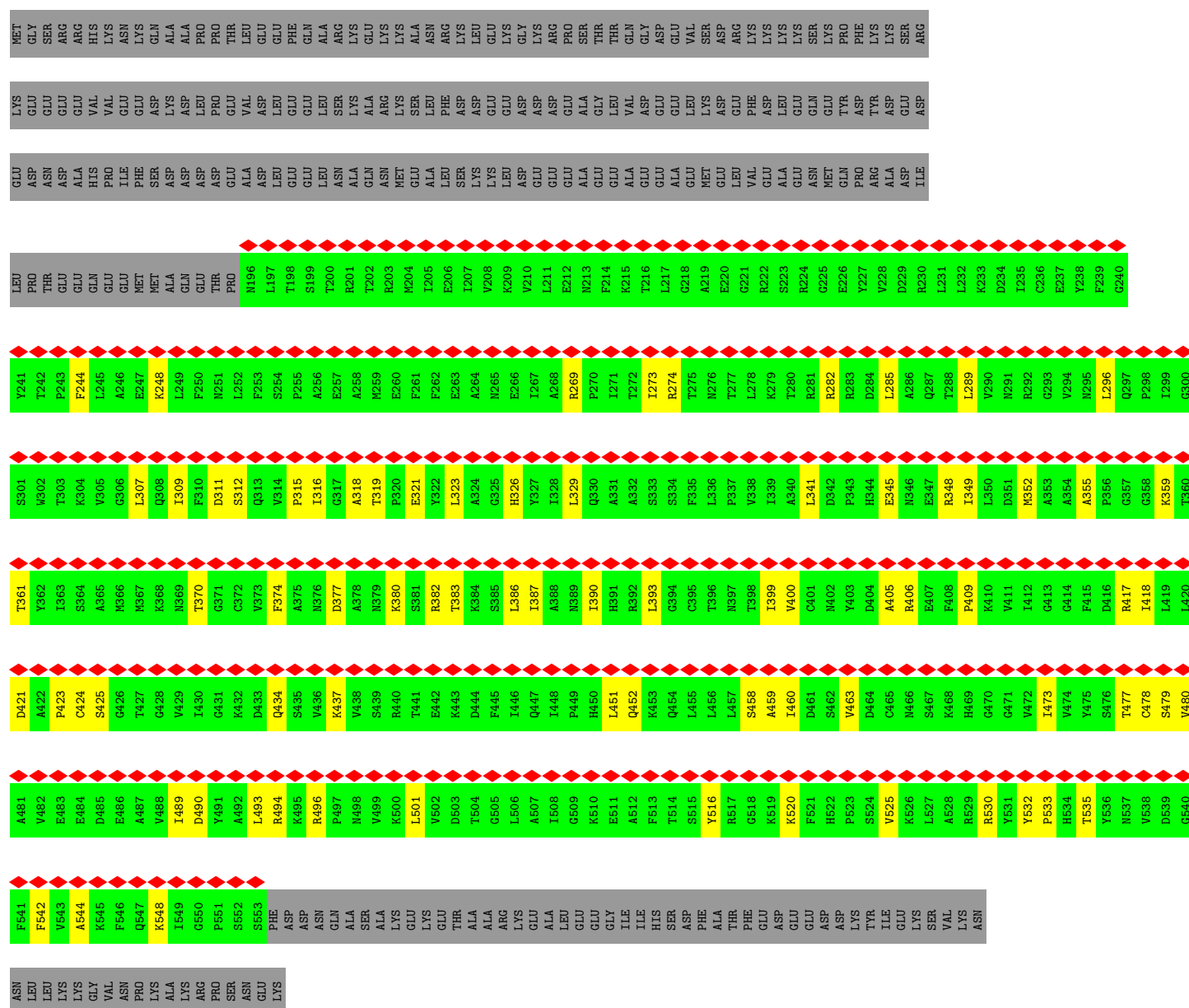
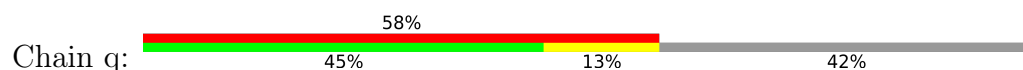
- Molecule 40: Ribosome biogenesis protein 15



MET	VAL	LYS	LYS	SER	THR	SER	LYS	THR	THR	LYS	GLU	THR	VAL	THR	THR	LYS	GLN	GLN	PRO	THR	THR	GLU	THR	GLU	GLY	GLY	LYS	LYS	GLY	GLU	GLY	LEU	ALA	ALA	LEU	GLU	THR	THR	SER	SER	SER	SER	SER	SER	ASP	GLY	GLU	GLU	GLU	GLU	ILE	GLY	GLY	GLY	LEU	ALA	ALA	ALA	SER	ASP	ASP	ASP	GLY	GLN
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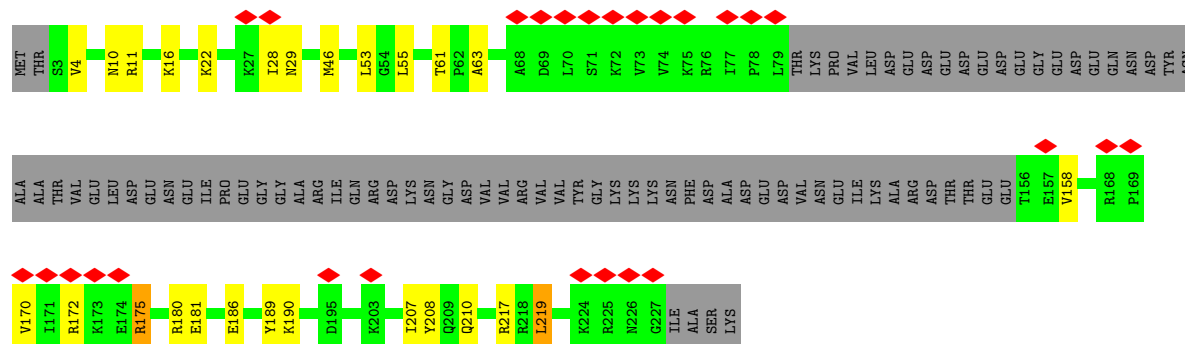
• Molecule 41: 25S rRNA (cytosine(2870)-C(5))-methyltransferase



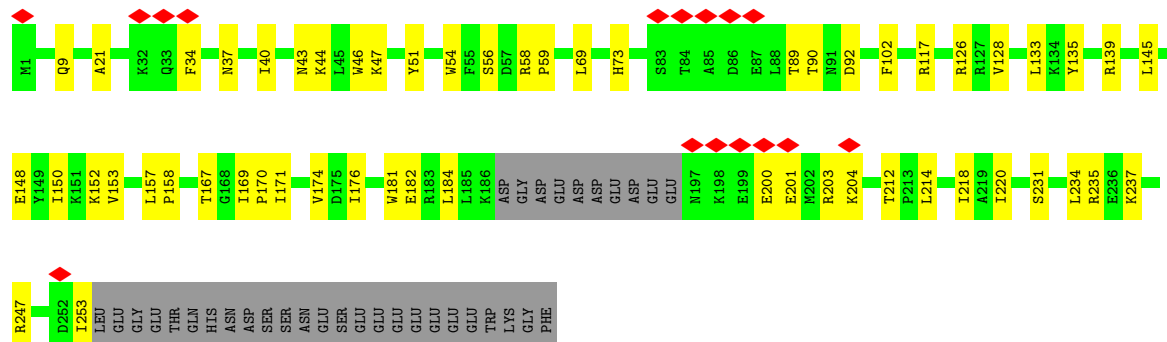
Chain r:



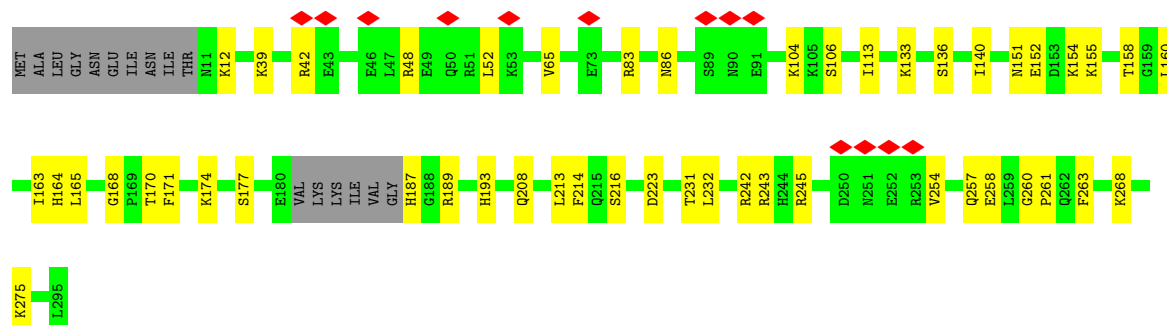
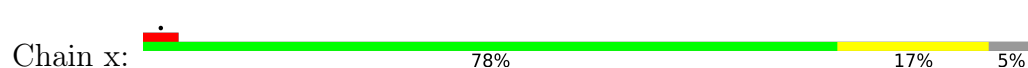
- Molecule 45: Nucleolar protein 16



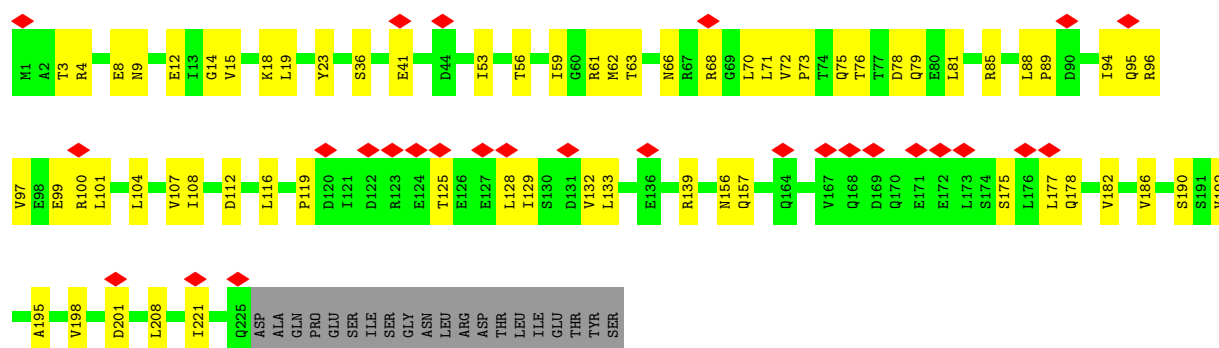
- Molecule 46: Ribosomal RNA-processing protein 1



- Molecule 47: Ribosome production factor 1



Chain y:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	374572	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	39.3	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.300	Depositor
Minimum map value	-0.185	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	444.78, 444.78, 444.78	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.059, 1.059, 1.059	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.21	0/48286	0.29	1/75246 (0.0%)
2	2	0.23	0/3562	0.29	0/5542
3	6	0.13	0/1367	0.25	0/2118
4	7	0.09	0/86	0.17	0/117
5	8	0.11	0/1210	0.24	0/1590
6	A	0.13	0/2126	0.27	0/2868
7	B	0.18	0/2679	0.31	0/3600
8	C	0.21	0/2660	0.34	0/3601
9	D	0.13	0/3441	0.26	0/4642
10	E	0.19	0/1226	0.31	0/1648
11	F	0.20	0/1974	0.33	0/2654
12	G	0.18	0/1294	0.34	0/1751
13	H	0.18	0/1523	0.31	0/2052
14	I	0.18	0/3182	0.33	0/4288
15	J	0.10	0/1289	0.23	0/1715
16	K	0.12	0/2190	0.27	0/2955
17	L	0.22	0/897	0.35	0/1205
18	M	0.18	0/1056	0.30	0/1421
19	N	0.20	0/1544	0.32	0/2065
20	O	0.21	0/1513	0.31	0/2029
21	P	0.18	0/1080	0.32	0/1455
22	Q	0.20	0/1127	0.31	0/1521
23	R	0.22	0/1609	0.34	0/2157
24	S	0.17	0/1468	0.30	0/1973
25	T	0.10	0/626	0.21	0/831
26	V	0.16	0/858	0.28	0/1156
27	W	0.12	0/1902	0.26	0/2564
28	Y	0.21	0/995	0.33	0/1329
29	Z	0.09	0/2051	0.23	0/2758
30	a	0.10	0/1695	0.25	0/2276
31	b	0.14	0/3495	0.29	0/4714
32	e	0.22	0/1039	0.38	0/1391

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.24	0/868	0.33	0/1168
34	h	0.18	0/978	0.32	0/1301
35	i	0.15	0/672	0.28	0/894
36	j	0.21	0/583	0.35	0/774
37	l	0.09	0/1425	0.23	0/1922
38	m	0.12	0/1806	0.26	0/2443
39	n	0.11	0/2828	0.25	0/3825
40	o	0.13	0/1129	0.27	0/1502
41	q	0.10	0/2854	0.25	0/3860
42	r	0.13	0/1508	0.24	0/2007
43	t	0.12	0/1999	0.29	0/2690
44	u	0.13	0/964	0.27	0/1283
45	v	0.15	0/1258	0.28	0/1670
46	w	0.18	0/2104	0.31	0/2832
47	x	0.20	0/2408	0.35	0/3230
48	y	0.16	0/1722	0.33	0/2343
All	All	0.19	0/126156	0.29	1/180976 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
17	L	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	406	G	O4'-C1'-N9	5.29	116.14	108.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	L	39	ARG	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	43147	0	21691	520	0
2	2	3189	0	1614	41	0
3	6	1227	0	622	19	0
4	7	87	0	101	2	0
5	8	1203	0	1291	16	0
6	A	2080	0	2100	31	0
7	B	2626	0	2705	42	0
8	C	2611	0	2724	38	0
9	D	3377	0	3500	38	0
10	E	1205	0	1291	15	0
11	F	1936	0	2032	21	0
12	G	1272	0	1331	20	0
13	H	1502	0	1564	21	0
14	I	3126	0	3178	41	0
15	J	1271	0	1310	16	0
16	K	2155	0	2230	29	0
17	L	884	0	936	16	0
18	M	1041	0	1137	17	0
19	N	1513	0	1564	30	0
20	O	1486	0	1588	19	0
21	P	1062	0	1075	15	0
22	Q	1110	0	1190	17	0
23	R	1578	0	1623	24	0
24	S	1432	0	1470	16	0
25	T	625	0	666	14	0
26	V	845	0	886	13	0
27	W	1870	0	1902	31	0
28	Y	984	0	1075	15	0
29	Z	2020	0	2105	42	0
30	a	1668	0	1753	21	0
31	b	3429	0	3484	65	0
32	e	1018	0	1086	19	0
33	f	850	0	880	11	0
34	h	969	0	1078	17	0
35	i	665	0	721	7	0
36	j	571	0	571	14	0
37	l	1394	0	1426	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	1759	0	1725	33	0
39	n	2760	0	2810	49	0
40	o	1107	0	1159	20	0
41	q	2799	0	2834	52	0
42	r	1489	0	1582	24	0
43	t	1973	0	2083	29	0
44	u	944	0	973	21	0
45	v	1242	0	1317	20	0
46	w	2058	0	2096	33	0
47	x	2362	0	2389	32	0
48	y	1701	0	1697	47	0
49	j	1	0	0	0	0
49	u	1	0	0	0	0
All	All	119224	0	98165	1437	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1437 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:W:45:LEU:HD13	27:W:48:VAL:CG1	1.71	1.19
41:q:460:ILE:O	41:q:463:VAL:HG12	1.46	1.14
31:b:192:VAL:CG2	31:b:201:THR:HG21	1.78	1.12
38:m:395:TYR:OH	39:n:33:ARG:HG2	1.46	1.12
27:W:45:LEU:O	27:W:45:LEU:HD12	1.49	1.10

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	7	9/204 (4%)	9 (100%)	0	0	100	100
5	8	139/434 (32%)	137 (99%)	2 (1%)	0	100	100
6	A	251/291 (86%)	245 (98%)	6 (2%)	0	100	100
7	B	327/387 (84%)	320 (98%)	7 (2%)	0	100	100
8	C	341/362 (94%)	334 (98%)	7 (2%)	0	100	100
9	D	417/505 (83%)	408 (98%)	9 (2%)	0	100	100
10	E	147/176 (84%)	144 (98%)	3 (2%)	0	100	100
11	F	239/244 (98%)	236 (99%)	3 (1%)	0	100	100
12	G	162/256 (63%)	153 (94%)	9 (6%)	0	100	100
13	H	187/191 (98%)	184 (98%)	3 (2%)	0	100	100
14	I	390/463 (84%)	384 (98%)	6 (2%)	0	100	100
15	J	149/427 (35%)	147 (99%)	2 (1%)	0	100	100
16	K	262/376 (70%)	253 (97%)	9 (3%)	0	100	100
17	L	108/199 (54%)	106 (98%)	2 (2%)	0	100	100
18	M	132/138 (96%)	129 (98%)	3 (2%)	0	100	100
19	N	173/204 (85%)	172 (99%)	1 (1%)	0	100	100
20	O	184/199 (92%)	182 (99%)	2 (1%)	0	100	100
21	P	133/184 (72%)	129 (97%)	4 (3%)	0	100	100
22	Q	142/186 (76%)	142 (100%)	0	0	100	100
23	R	188/306 (61%)	186 (99%)	2 (1%)	0	100	100
24	S	168/172 (98%)	163 (97%)	5 (3%)	0	100	100
25	T	77/250 (31%)	76 (99%)	1 (1%)	0	100	100
26	V	110/137 (80%)	109 (99%)	1 (1%)	0	100	100
27	W	230/236 (98%)	221 (96%)	9 (4%)	0	100	100
28	Y	123/127 (97%)	121 (98%)	2 (2%)	0	100	100
29	Z	247/453 (54%)	243 (98%)	4 (2%)	0	100	100
30	a	208/217 (96%)	197 (95%)	11 (5%)	0	100	100
31	b	417/647 (64%)	404 (97%)	13 (3%)	0	100	100
32	e	124/130 (95%)	122 (98%)	2 (2%)	0	100	100
33	f	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
34	h	117/120 (98%)	116 (99%)	1 (1%)	0	100	100
35	i	82/100 (82%)	79 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	j	70/88 (80%)	67 (96%)	3 (4%)	0	100	100
37	l	174/181 (96%)	171 (98%)	3 (2%)	0	100	100
38	m	205/807 (25%)	201 (98%)	4 (2%)	0	100	100
39	n	329/605 (54%)	319 (97%)	10 (3%)	0	100	100
40	o	131/220 (60%)	126 (96%)	5 (4%)	0	100	100
41	q	356/618 (58%)	349 (98%)	7 (2%)	0	100	100
42	r	174/261 (67%)	171 (98%)	3 (2%)	0	100	100
43	t	245/322 (76%)	240 (98%)	5 (2%)	0	100	100
44	u	110/199 (55%)	108 (98%)	2 (2%)	0	100	100
45	v	145/231 (63%)	140 (97%)	5 (3%)	0	100	100
46	w	239/278 (86%)	232 (97%)	7 (3%)	0	100	100
47	x	275/295 (93%)	264 (96%)	11 (4%)	0	100	100
48	y	223/245 (91%)	211 (95%)	12 (5%)	0	100	100
All	All	8763/12778 (69%)	8552 (98%)	211 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	7	11/181 (6%)	11 (100%)	0	100	100
5	8	128/388 (33%)	128 (100%)	0	100	100
6	A	232/263 (88%)	231 (100%)	1 (0%)	84	92
7	B	278/323 (86%)	276 (99%)	2 (1%)	76	89
8	C	273/289 (94%)	272 (100%)	1 (0%)	84	92
9	D	371/440 (84%)	371 (100%)	0	100	100
10	E	131/153 (86%)	130 (99%)	1 (1%)	73	88
11	F	204/205 (100%)	204 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	G	133/208 (64%)	131 (98%)	2 (2%)	57	79
13	H	169/171 (99%)	169 (100%)	0	100	100
14	I	352/410 (86%)	352 (100%)	0	100	100
15	J	139/383 (36%)	138 (99%)	1 (1%)	76	89
16	K	247/346 (71%)	246 (100%)	1 (0%)	84	92
17	L	89/159 (56%)	88 (99%)	1 (1%)	65	83
18	M	106/109 (97%)	106 (100%)	0	100	100
19	N	153/176 (87%)	150 (98%)	3 (2%)	48	73
20	O	153/162 (94%)	149 (97%)	4 (3%)	40	66
21	P	109/146 (75%)	107 (98%)	2 (2%)	51	75
22	Q	118/151 (78%)	114 (97%)	4 (3%)	32	57
23	R	171/274 (62%)	171 (100%)	0	100	100
24	S	155/156 (99%)	154 (99%)	1 (1%)	78	90
25	T	69/219 (32%)	68 (99%)	1 (1%)	59	80
26	V	88/105 (84%)	88 (100%)	0	100	100
27	W	209/213 (98%)	207 (99%)	2 (1%)	68	85
28	Y	108/110 (98%)	106 (98%)	2 (2%)	50	74
29	Z	234/413 (57%)	233 (100%)	1 (0%)	84	92
30	a	191/198 (96%)	190 (100%)	1 (0%)	81	91
31	b	380/573 (66%)	373 (98%)	7 (2%)	51	75
32	e	109/111 (98%)	108 (99%)	1 (1%)	70	86
33	f	90/91 (99%)	89 (99%)	1 (1%)	65	83
34	h	104/105 (99%)	102 (98%)	2 (2%)	50	74
35	i	70/82 (85%)	70 (100%)	0	100	100
36	j	59/71 (83%)	58 (98%)	1 (2%)	53	77
37	l	151/156 (97%)	150 (99%)	1 (1%)	76	89
38	m	193/723 (27%)	191 (99%)	2 (1%)	68	85
39	n	305/548 (56%)	301 (99%)	4 (1%)	61	81
40	o	118/199 (59%)	116 (98%)	2 (2%)	53	77
41	q	304/535 (57%)	303 (100%)	1 (0%)	86	94
42	r	163/229 (71%)	162 (99%)	1 (1%)	78	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	t	220/287 (77%)	217 (99%)	3 (1%)	59	80
44	u	98/180 (54%)	96 (98%)	2 (2%)	48	73
45	v	134/205 (65%)	130 (97%)	4 (3%)	36	62
46	w	225/257 (88%)	223 (99%)	2 (1%)	70	86
47	x	263/276 (95%)	258 (98%)	5 (2%)	50	74
48	y	193/211 (92%)	192 (100%)	1 (0%)	81	91
All	All	7800/11190 (70%)	7729 (99%)	71 (1%)	68	86

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	u	22	VAL
45	v	28	ILE
47	x	65	VAL
25	T	232	VAL
24	S	172	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
23	R	17	HIS
48	y	11	ASN
29	Z	171	ASN
42	r	13	GLN
27	W	91	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1993/3396 (58%)	396 (19%)	5 (0%)
2	2	147/158 (93%)	28 (19%)	0
3	6	54/232 (23%)	19 (35%)	0
All	All	2194/3786 (57%)	443 (20%)	5 (0%)

5 of 443 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U

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Mol	Chain	Res	Type
1	1	5	G
1	1	48	A
1	1	49	A
1	1	59	G

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1886	A
1	1	2420	C
1	1	2889	C
1	1	3121	U
1	1	3386	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

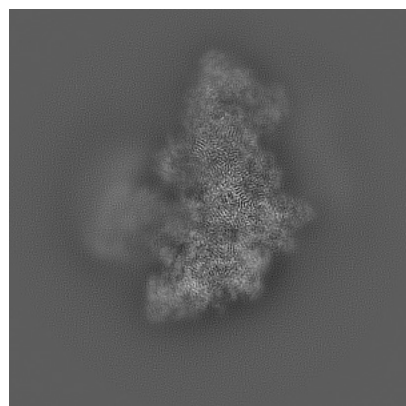
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43017. These allow visual inspection of the internal detail of the map and identification of artifacts.

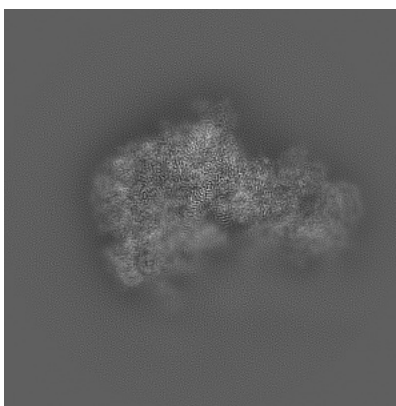
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

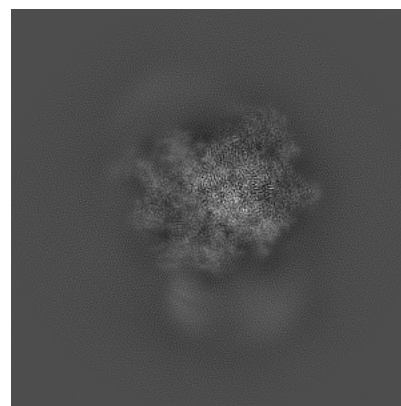
6.1.1 Primary map



X

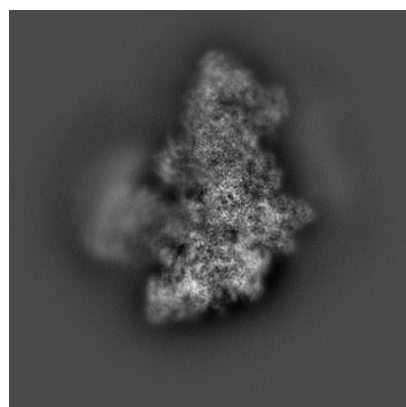


Y

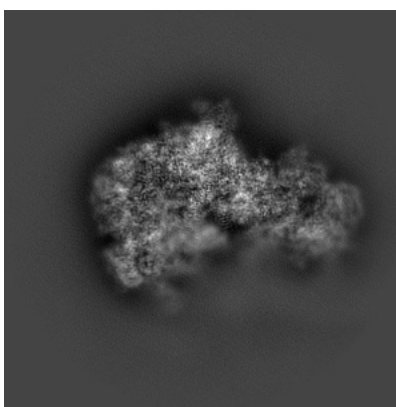


Z

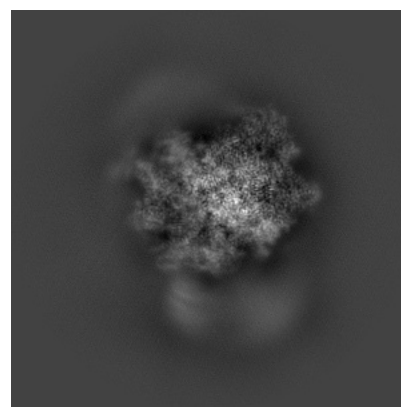
6.1.2 Raw map



X



Y

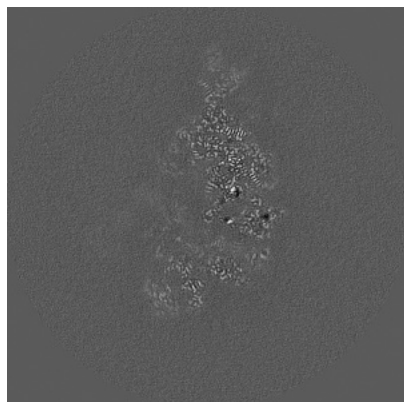


Z

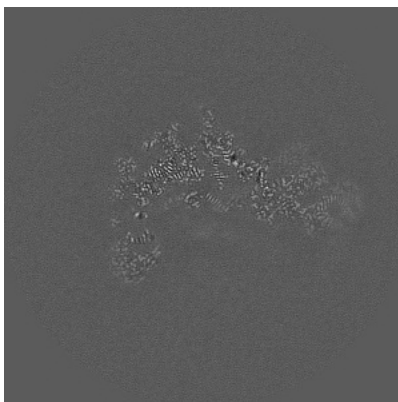
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

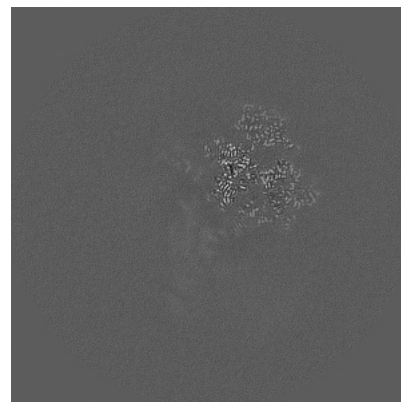
6.2.1 Primary map



X Index: 210

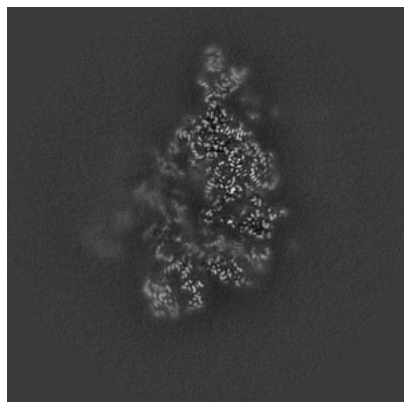


Y Index: 210

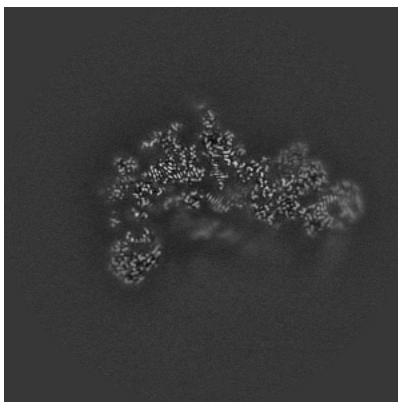


Z Index: 210

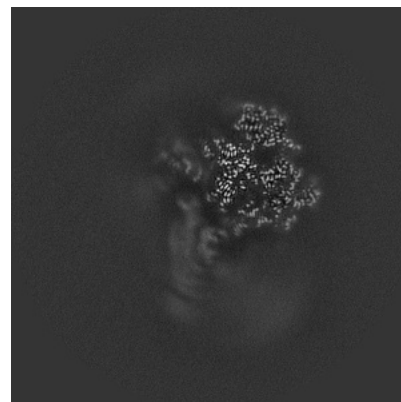
6.2.2 Raw map



X Index: 210



Y Index: 210

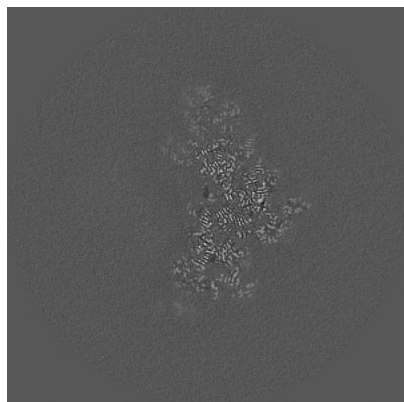


Z Index: 210

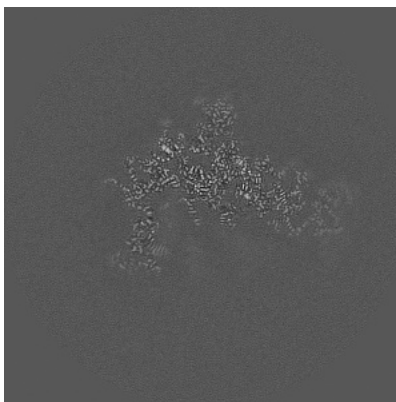
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

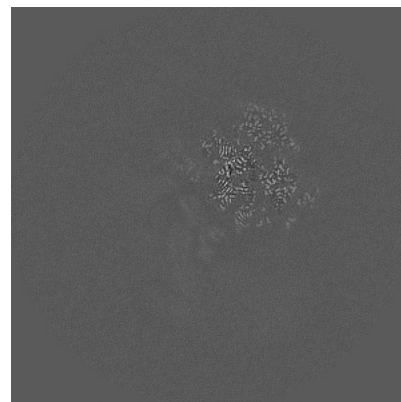
6.3.1 Primary map



X Index: 246

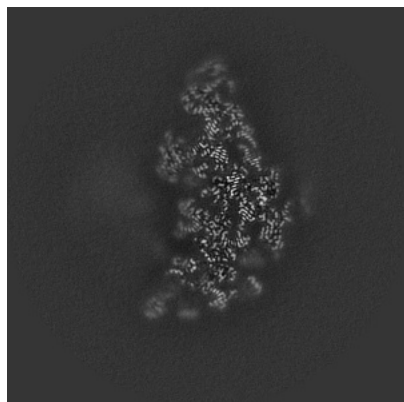


Y Index: 228

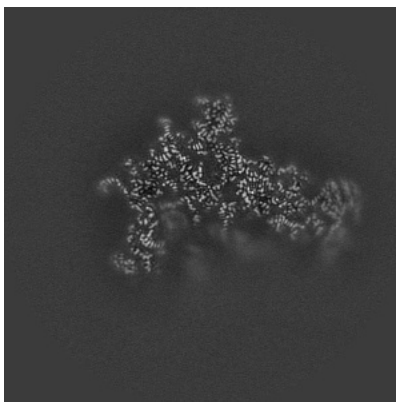


Z Index: 207

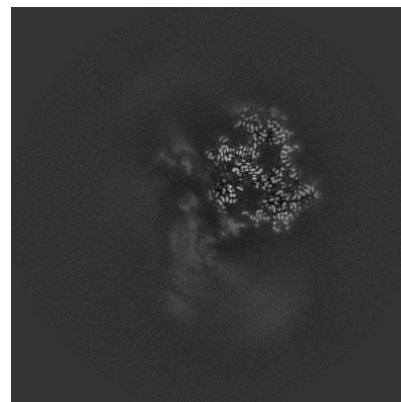
6.3.2 Raw map



X Index: 237



Y Index: 225

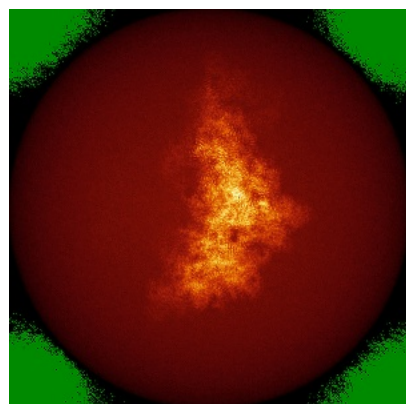


Z Index: 214

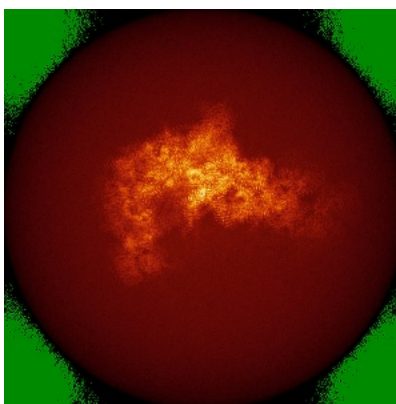
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

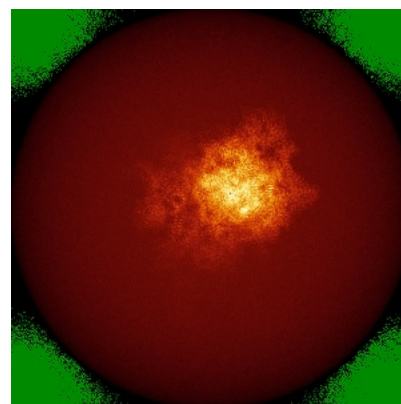
6.4.1 Primary map



X



Y



Z

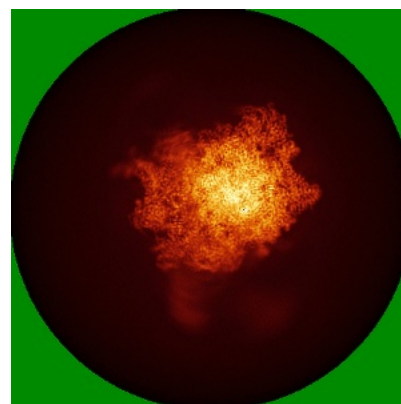
6.4.2 Raw map



X



Y

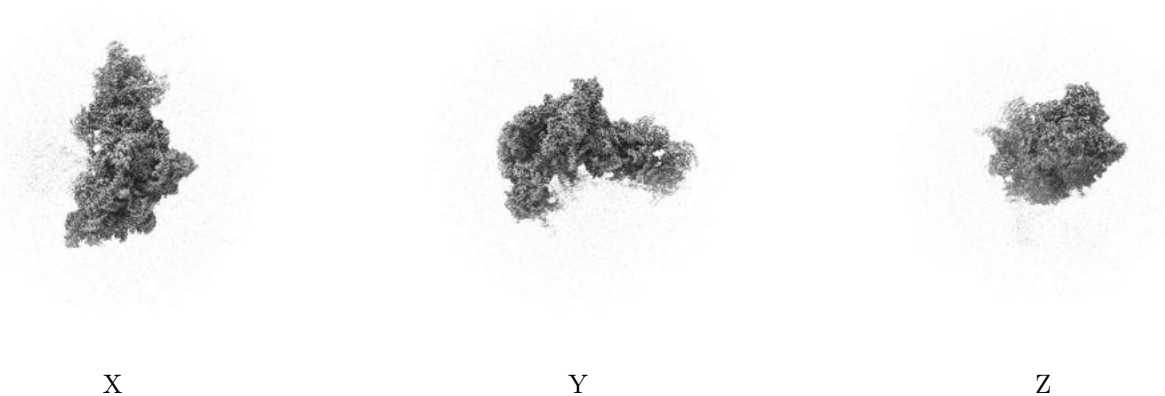


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

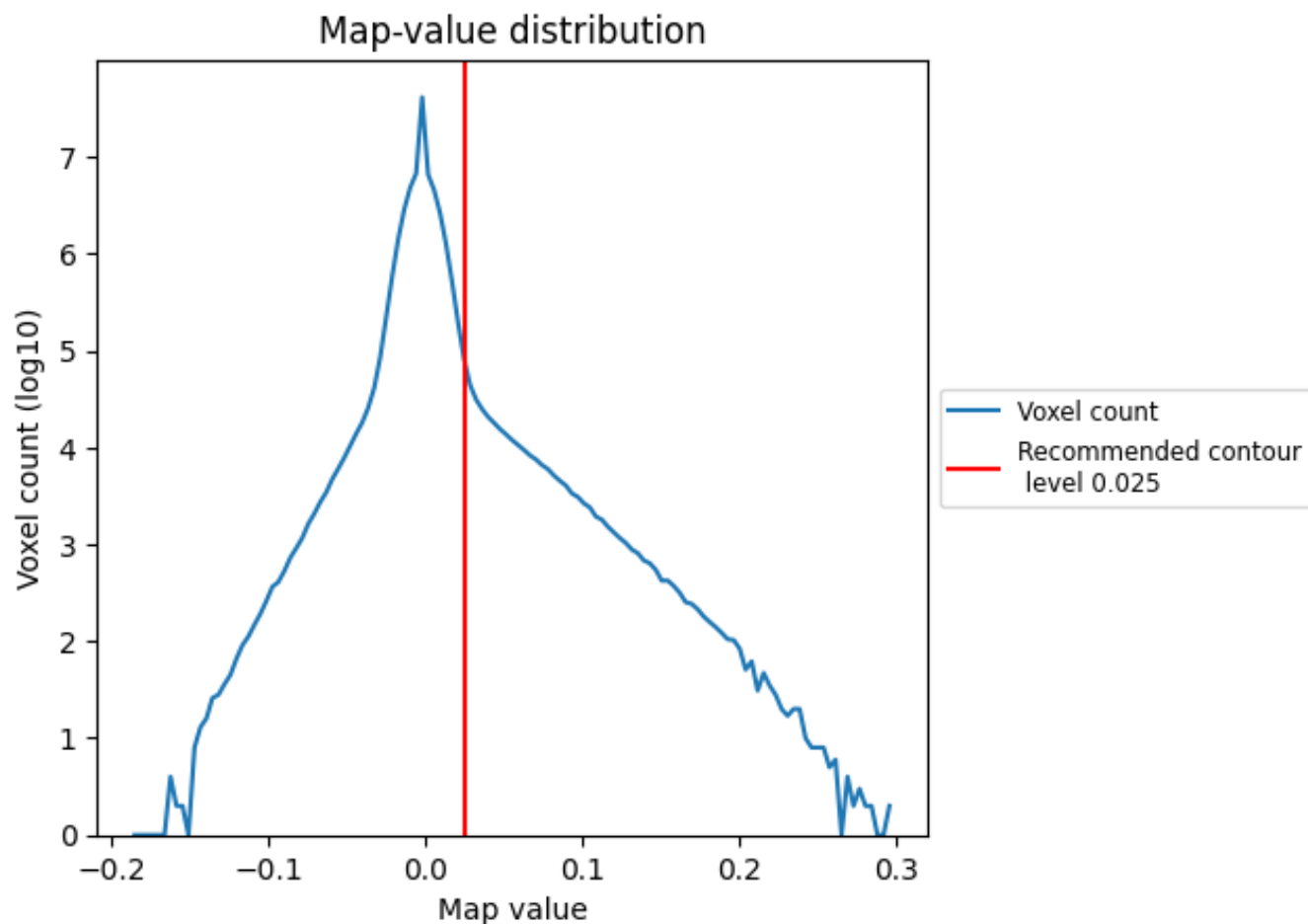
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

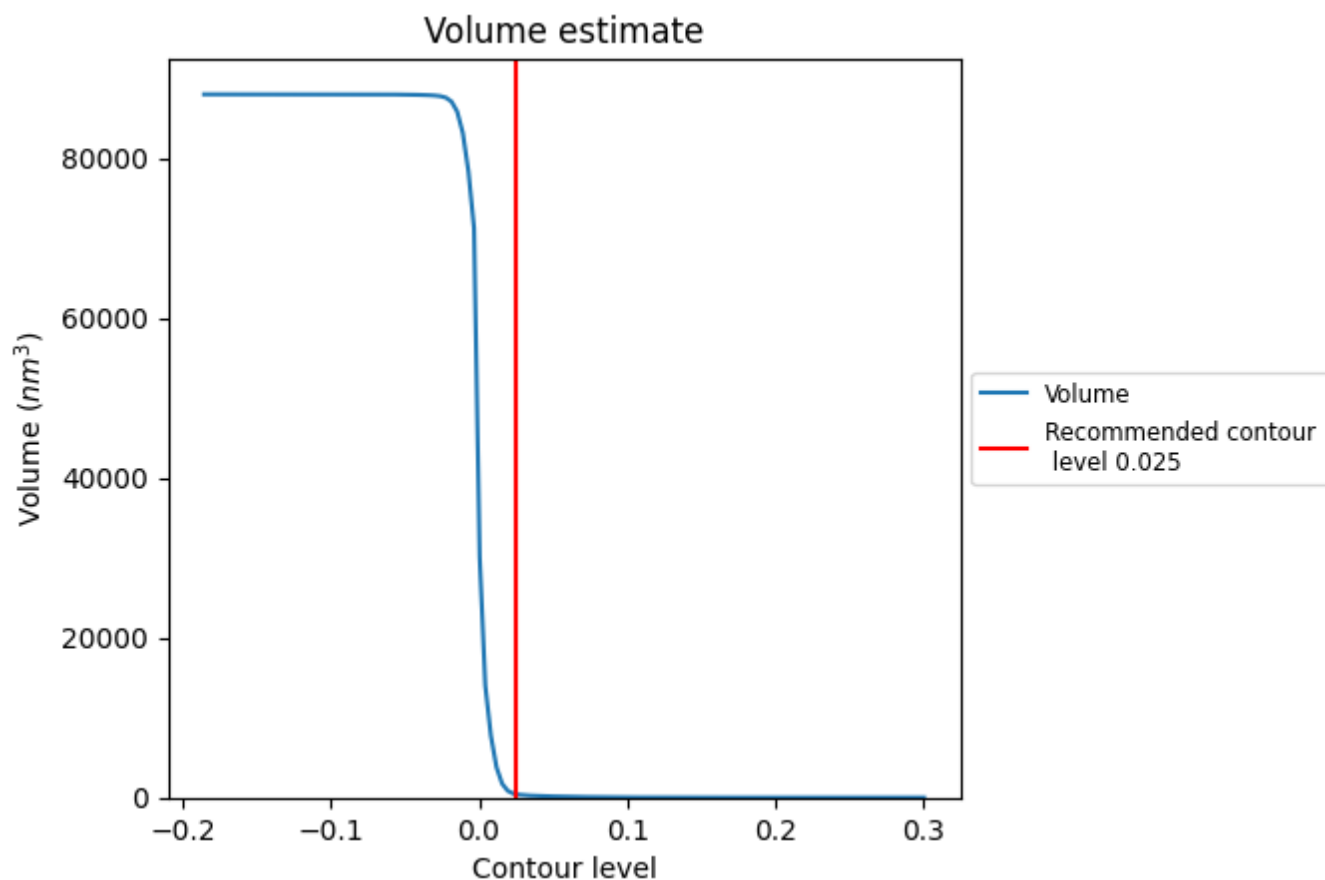
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

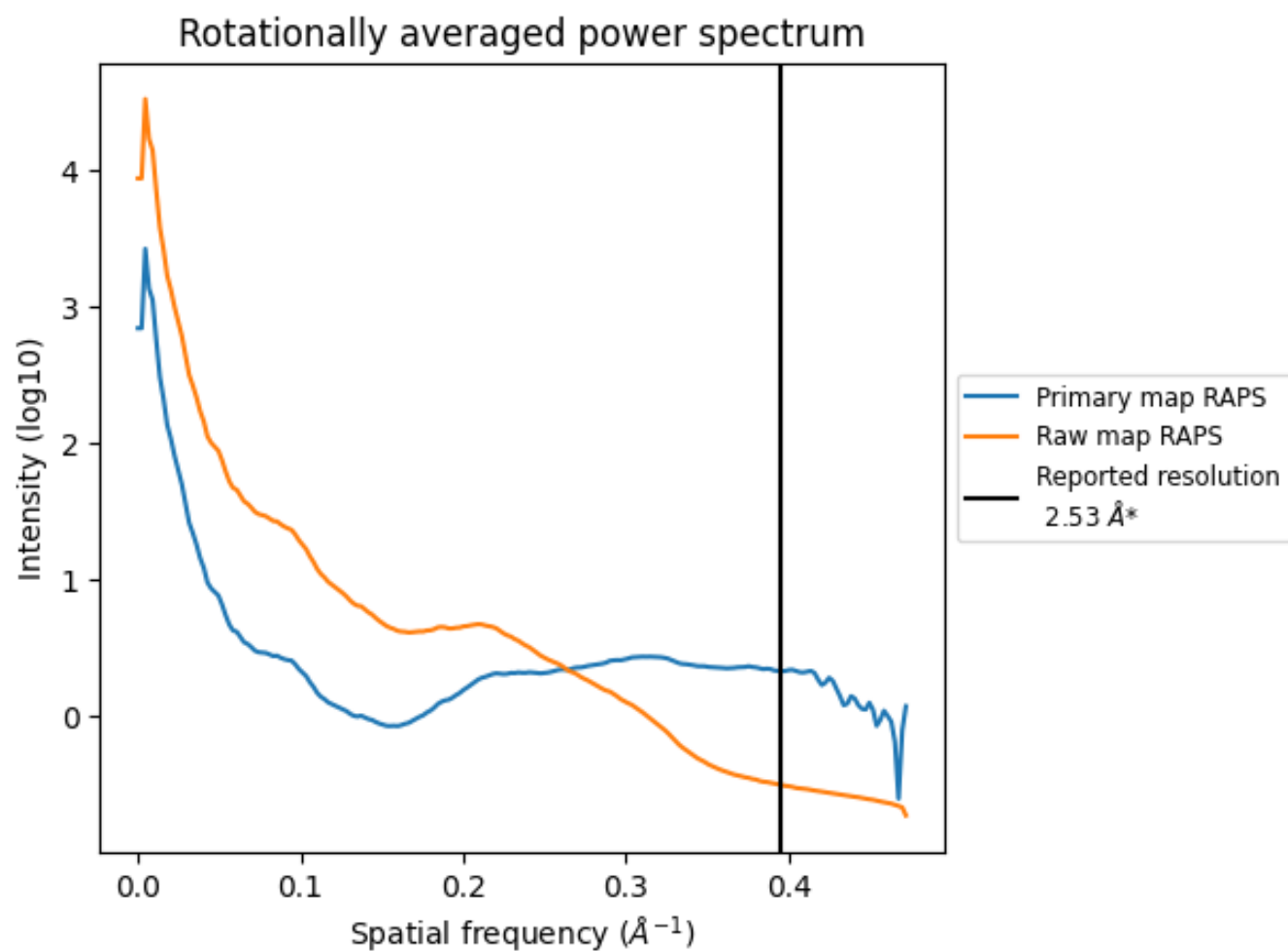
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 427 nm^3 ; this corresponds to an approximate mass of 386 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

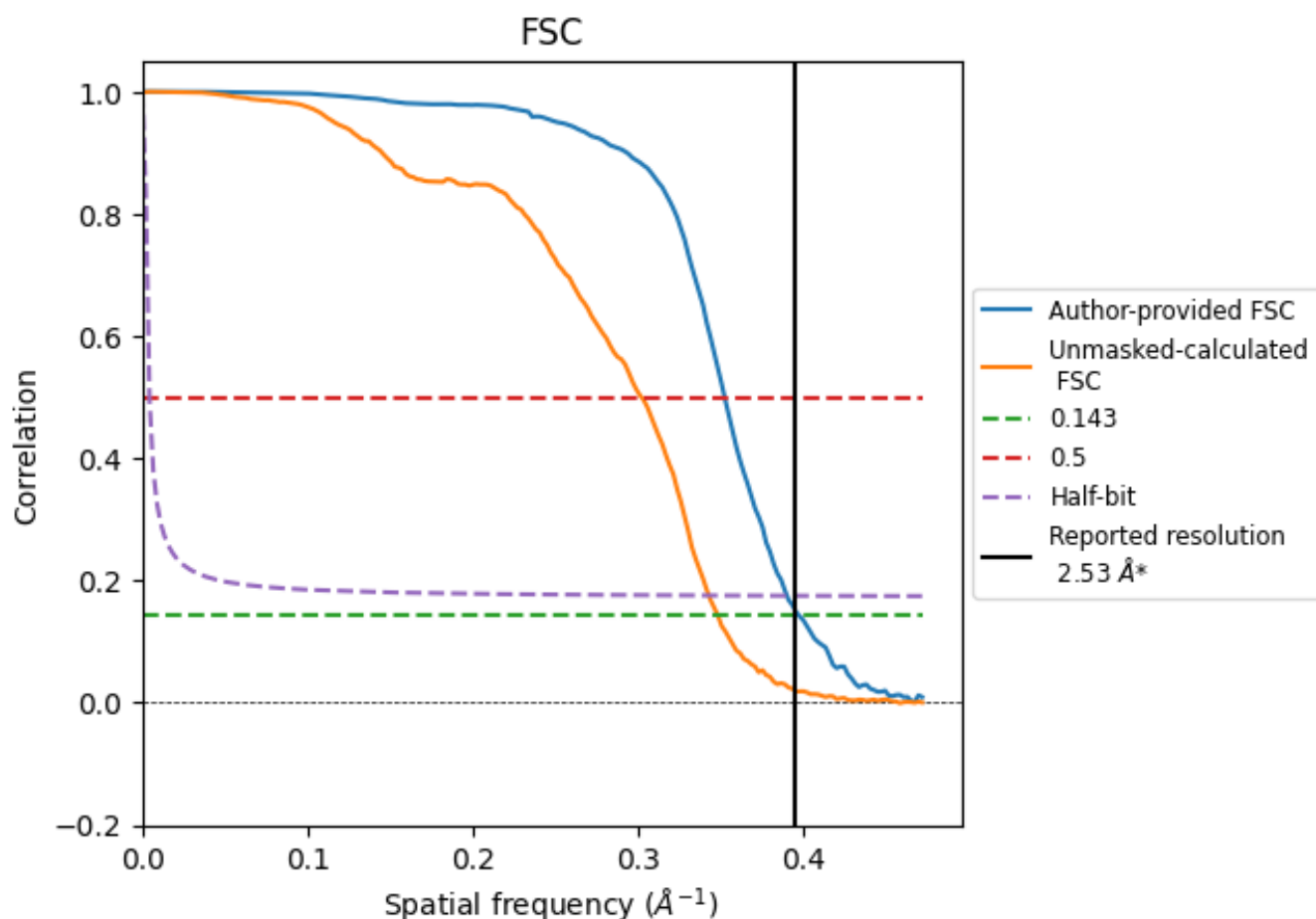


*Reported resolution corresponds to spatial frequency of 0.395 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.395 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.53	-	-
Author-provided FSC curve	2.52	2.84	2.56
Unmasked-calculated*	2.87	3.31	2.92

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.87 differs from the reported value 2.53 by more than 10 %

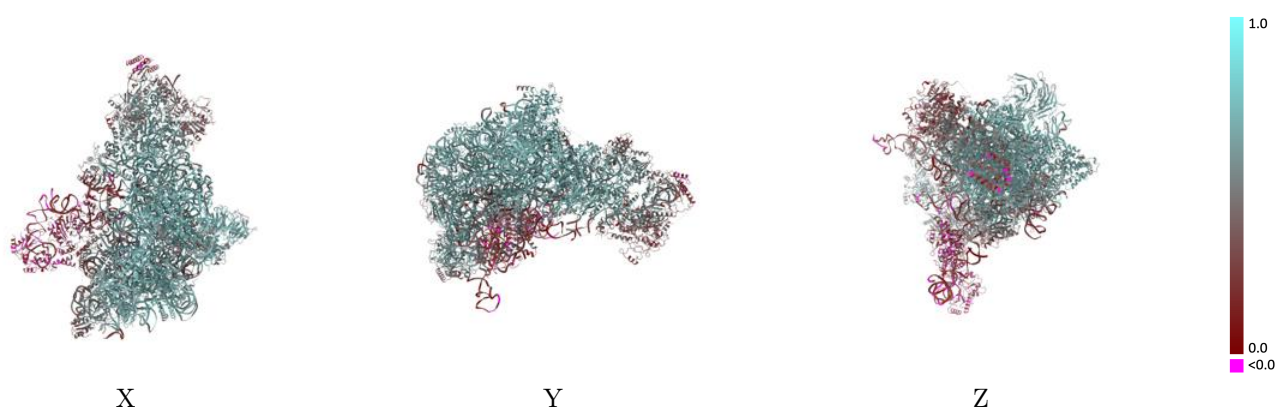
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43017 and PDB model 8V83. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)

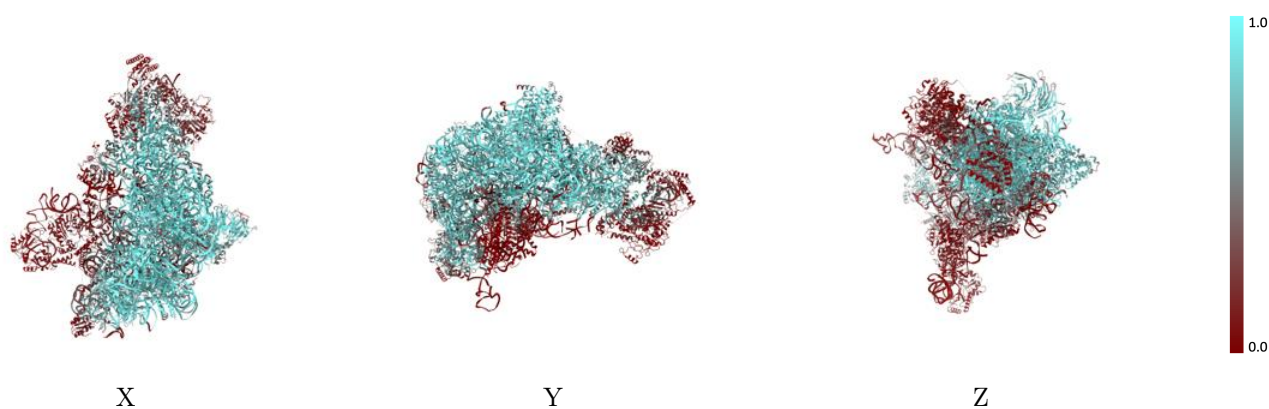
This section was not generated.

9.2 Q-score mapped to coordinate model [i](#)



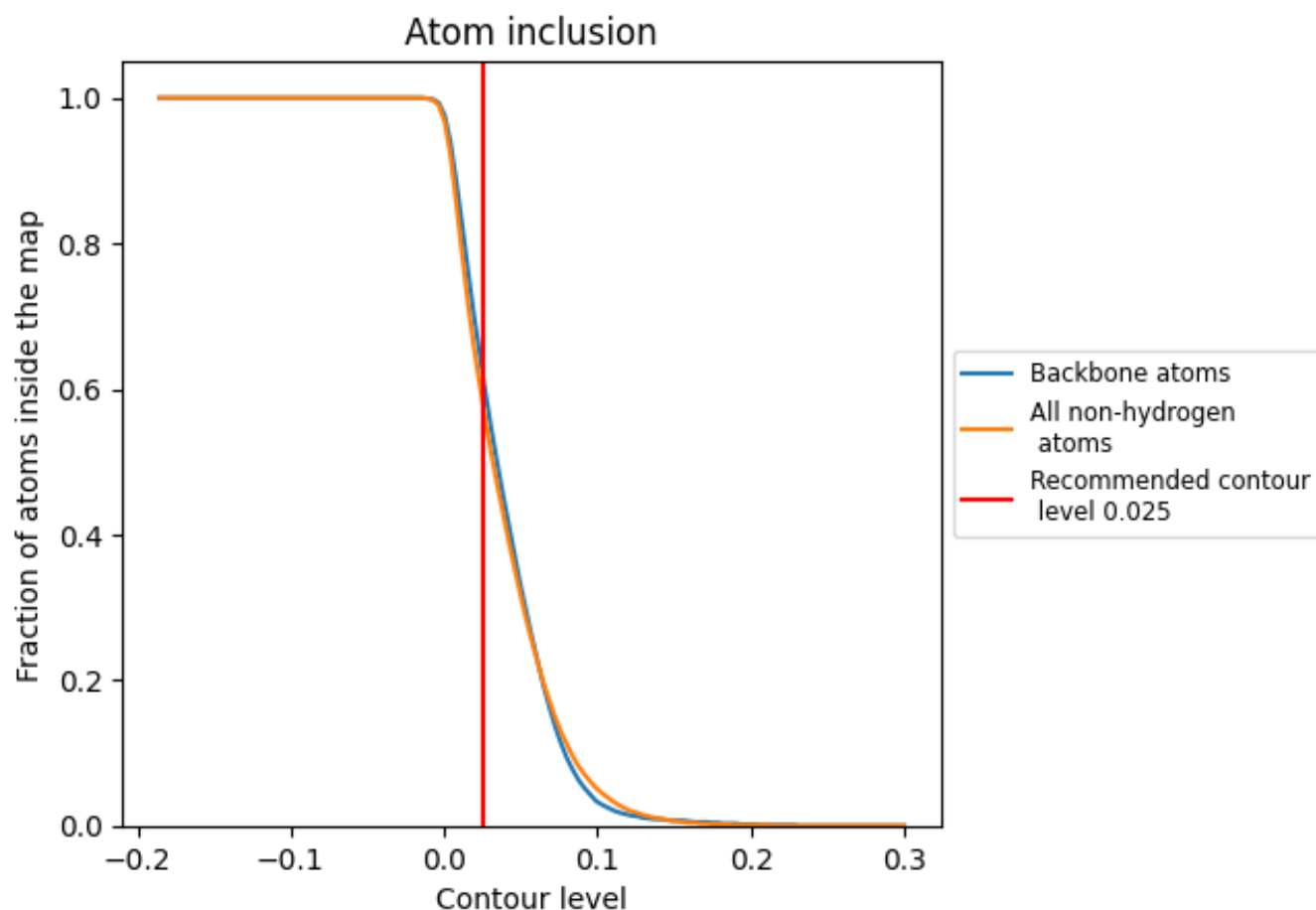
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5830	 0.5300
1	 0.6480	 0.5310
2	 0.7780	 0.6090
6	 0.4710	 0.4920
7	 0.0000	 0.1490
8	 0.2450	 0.4480
A	 0.4400	 0.5340
B	 0.7660	 0.6210
C	 0.9430	 0.7060
D	 0.3700	 0.5020
E	 0.8420	 0.6540
F	 0.8750	 0.6720
G	 0.8170	 0.6480
H	 0.7820	 0.6360
I	 0.7930	 0.6450
J	 0.0890	 0.3730
K	 0.2360	 0.4210
L	 0.8890	 0.6820
M	 0.8580	 0.6640
N	 0.8160	 0.6540
O	 0.8440	 0.6680
P	 0.7870	 0.6530
Q	 0.8930	 0.6820
R	 0.8700	 0.6810
S	 0.7080	 0.6190
T	 0.0020	 0.2290
V	 0.7060	 0.5970
W	 0.2570	 0.4550
Y	 0.8870	 0.6900
Z	 0.0070	 0.2720
a	 0.0000	 0.1330
b	 0.3790	 0.4920
e	 0.9260	 0.6990
f	 0.9290	 0.7010
h	 0.6650	 0.6070



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Chain	Atom inclusion	Q-score
i	 0.6680	 0.6010
j	 0.9140	 0.6930
l	 0.0010	 0.1510
m	 0.2710	 0.4340
n	 0.1620	 0.3940
o	 0.3630	 0.4340
q	 0.0020	 0.1470
r	 0.3540	 0.4950
t	 0.2530	 0.4450
u	 0.5420	 0.5320
v	 0.6850	 0.6060
w	 0.8080	 0.6390
x	 0.8300	 0.6550
y	 0.6770	 0.5810